

## RESULT 4

US-10-311-034-7  
; Sequence 7, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YOE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: GREENWALD, Sara R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: KEARNEY, Liam  
; APPLICANT: BURFORD, Neil  
; APPLICANT: NGUYEN, Dannel B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAFALIA, April  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKY, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GREYER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeev  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
; 60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 7  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1  
US-10-311-034-7

Query Match 99.5%; Score 2589; DB 15; Length 497;  
Best Local Similarity 99.6%; Pred. No. 1.8e-183;  
Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAEPIANRSLNLFPGKPEFTQOQMSPLSREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAEPIANRSLNLFPGKPEFTQOQMSPLSREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSFNVRKYSPTIAELQELQPSAKDFEVSILVGCGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNVRKYSPTIAELQELQPSAKDFEVSILVGCGHFAEVQVVRKATG 120

Qy 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
Qy 181 DLLSLNRYEDQDENLQFYLAELILAVSHVHMGYVHRDIKPNILVDRFGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLQFYLAELILAVSHVHMGYVHRDIKPNILVDRFGHIKLVDF 240  
Qy 241 GSAAKXNSNKNVNAKLPICTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAIYEMIXGR 300  
Db 241 GSAAKXNSNKNVNAKLPICTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAIYEMIXGR 300  
Qy 301 SPFAEGTSARTFNININFORFLKFPDDPKVSSDFDLQSLCCGKERLKFGLCHPFF 360  
Db 301 SPFAEGTSARTFNININFORFLKFPDDPKVSSDFDLQSLCCGKERLKFGLCHPFF 360  
Qy 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDEPKNSWVSSPQQLSPSGSGSELFPVGF 420  
Db 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDEPKNSWVSSPQQLSPSGSGSELFPVGF 420  
Qy 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
Qy 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

## RESULT 5

US-10-262-511-4  
; Sequence 4, Application US/10262511  
; Publication No. US20040038223A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Ju, Jinfang  
; APPLICANT: Li, Li  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Spytex, Kimberly A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyavkar, Uriel M.  
; APPLICANT: Ort, Tatiana  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zerkisen, Bryan D.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Stone, David J.  
; APPLICANT: Pina, Carol E. A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Hochenberg, Mark E.  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Agee, Michele L.  
; APPLICANT: Berghs, Constance  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-462C  
; CURRENT APPLICATION NUMBER: US/10/262,511  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/373,815  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09

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Db 661 CATCGAGCATCAAGCCTGAGACATTCCTGTTGACCGCAGAGACATCAAGCTGTG 720  
 Qy 721 GATTTTGGATTCGCGCGAAATGAATCAACAGATGTGTAATGCCAACTCCCGATT 780  
 Db 721 GATTTTGGATTCGCGCGAAATGAATCAACAGATGTGTAATGCCAACTCCCGATT 780  
 Qy 781 GGGACCCAGATTACATGCTCCCTCAAGTGTGACTGTGATGAGCGGGGATGGAAGGC 840  
 Db 781 GGGACCCAGATTACATGCTCCCTCAAGTGTGACTGTGATGAGCGGGGATGGAAGGC 840  
 Qy 841 ACCTAGCGCTGGACTGTGACTGTGTTAGTGGCGGTGATGCTATGAGATGATTAT 900  
 Db 841 ACCTAGCGCTGGACTGTGACTGTGTTAGTGGCGGTGATGCTATGAGATGATTAT 900  
 Qy 901 GGGATCCCTTCGCGAGAGGAACTCTCCGAGAACCTTCGCGAGACCTTCAATAACATTATGATTC 960  
 Db 901 GGGATCCCTTCGCGAGAGGAACTCTTCGCGAGAACCTTCGCGAGACCTTCAATAACATTATGATTC 960  
 Qy 961 CAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTGCTGCCATCCT 1020  
 Db 961 CAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTGCTGCCATCCT 1020  
 Qy 1021 CAAGCTTTGTTGGCGGCGAGAGAGAGACTGAAGTTGAAGTCTTTGCTGCCATCCT 1080  
 Db 1021 CAAGCTTTGTTGGCGGCGAGAGAGAGACTGAAGTTGAAGTCTTTGCTGCCATCCT 1080  
 Qy 1081 TTCTTCTAAATTTGACTGAACCAATTCGTAACCTCTCCCGGCTTCGTTCCACC 1140  
 Db 1081 TTCTTCTAAATTTGACTGAACCAATTCGTAACCTCTCCCGGCTTCGTTCCACC 1140  
 Qy 1141 CTCAGTCCGACGATGACCTCCAAATTTGATGAACAGAGAGAAATTCGTTGGTTCA 1200  
 Db 1141 CTCAGTCCGACGATGACCTCCAAATTTGATGAACAGAGAGAAATTCGTTGGTTCA 1200  
 Qy 1201 TCCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGTCGAGAACTGCGGTTGGGG 1260  
 Db 1201 TCCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGTCGAGAACTGCGGTTGGGG 1260  
 Qy 1261 TTTTCGTACAGCAAGGACCTGGGATTCCTTGGTAGATCTGAGTCTGTTGTCGGGCTG 1320  
 Db 1261 TTTTCGTACAGCAAGGACCTGGGATTCCTTGGTAGATCTGAGTCTGTTGTCGGGCTG 1320  
 Qy 1321 GACTCCCTCCGACGACTAGCTCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1321 GACTCCCTCCGACGACTAGCTCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Qy 1381 CAAGACTCTCAGGACAGTGTCAAGGTATTTATTTCCGACCGCGCTCTCTCTCTG 1440  
 Db 1381 CAAGACTCTCAGGACAGTGTCAAGGTATTTATTTCCGACCGCGCTCTCTCTCTG 1440  
 Qy 1441 TCCAGGATCTCCCGTCCGTTATATGCAAGGGATCCCGCGCGGCGCTGCTGCTCTGA 1500  
 Db 1441 TCCAGGATCTCCCGTCCGTTATATGCAAGGGATCCCGCGCGGCGCTGCTGCTCTGA 1500  
 Qy 1501 GCGGCTGATCCGTA 1515  
 Db 1501 GCGGCTGATCCGTA 1515

RESULT 4

US-10-311-034-33  
 ; Sequence 33, Application US/10311034  
 ; Publication No. US2004002342A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.  
 ; APPLICANT: YUE, Henry  
 ; APPLICANT: LAL, Preeti  
 ; APPLICANT: BANDMAN, Olga  
 ; APPLICANT: BOROWSKY, Mark L.  
 ; APPLICANT: AU-YOUNG, Janice  
 ; APPLICANT: LU, Yan  
 ; APPLICANT: GANDHI, Ameena R.

APPLICANT: TRIBOULEY, Catherine M.  
 APPLICANT: CHAWLA, Narinder K.  
 APPLICANT: YAO, Monique G.  
 APPLICANT: LU, Dyung Aina M.  
 APPLICANT: GREENWALD, Sara R.  
 APPLICANT: RAMKUMAR, Jayalaxmi  
 APPLICANT: GRIFFIN, Jennifer A.  
 APPLICANT: KEARNEY, Liam  
 APPLICANT: BURFORD, Neil  
 APPLICANT: NGUYEN, Dannie B.  
 APPLICANT: TANG, Y. Tom  
 APPLICANT: BAUGHN, Mariah R.  
 APPLICANT: HE, Ann  
 APPLICANT: THORNTON, Michael  
 APPLICANT: HAFALIA, April  
 APPLICANT: ARVIZU, Chandra S.  
 APPLICANT: GURURAJAN, Rajagopal  
 APPLICANT: LO, Terence P.  
 APPLICANT: KHAN, Farrah A.  
 APPLICANT: RECIPON, Shirley A.  
 APPLICANT: AZIMZAI, Yalda  
 APPLICANT: POLICKY, Jennifer L.  
 APPLICANT: DING, Li  
 APPLICANT: GREYER, Megan  
 APPLICANT: ELLIOTT, Vicki S.  
 APPLICANT: THANGAVELU, Kavitha  
 APPLICANT: BATRA, Sajeev  
 APPLICANT: ISON, Craig H.  
 TITLE OF INVENTION: HUMAN KINASES  
 FILE REFERENCE: PI-0125 PCT  
 CURRENT APPLICATION NUMBER: US/10/311,034  
 PRIOR FILING DATE: 2002-12-10  
 PRIOR APPLICATION NUMBER: 60/213,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
 60/228,056  
 PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0-  
 25  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: PERL Program  
 SEQ ID NO 33  
 LENGTH: 2056  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Incyte ID No. US2004002342A1 3951059CB1  
 US-10-311-034-33

Query Match 99.7%; Score 1510.2; DB 16; Length 2066;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GGGGAGATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 60  
 Db 8 GGGGAGATGTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 67  
 Qy 61 CCCATTGCCAACCGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAACACACCTTTATG 120  
 Db 68 CCCATTGCCAGCGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAACACACCTTTATG 127  
 Qy 121 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
 Db 128 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 187  
 Qy 181 TTTGAAGAATGCAGTCTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG 240  
 Db 188 TTTGAAGAATGCAGTCTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG 247  
 Qy 241 AAGTATTCGACACCATAGCTAGTTACAGGAGCTCCAGCTTCGCAAGAGACTTCGAA 300  
 Db 248 AAGTATTCGACACCATAGCTAGTTACAGGAGCTCCAGCTTCGCAAGAGACTTCGAA 307  
 Qy 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAGTGCAGGTGCTAGAGAGAGCA 360

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308 GTCAAGAGCTCTTAGGTTGGTCTACTTCTGCTGAGTGGAGGTTAAGAGAGAGCA 367  
 361 ACCGGGACATCTATGCTATGAAGTGTAGTGAAGAGAGGCTTTATTTGGCCCGAGGACG 420  
 368 ACCGGGACATCTATGCTATGAAGTGTAGTGAAGAGAGGCTTTATTTGGCCCGAGGACG 427  
 421 GTTTCATTTTGGAGAGAGGAGGACATATATCTCAAGCAACAAGCCCGTGGATCCCC 480  
 428 GTTTCATTTTGGAGAGAGGAGGACATATATCTCAAGCAACAAGCCCGTGGATCCCC 487  
 481 CAATTACAGTATGCTCTTTCAGGACAAAATCACTTTTATCTGGTCAATGGAATATCAGCCT 540  
 488 CAATTACAGTATGCTCTTTCAGGACAAAATCACTTTTATCTGGTCAATGGAATATCAGCCT 547  
 541 GGGGGGACTCTGCTGCTCTTTGATAGATAGTGAAGAGGCTTTAGTGAAGAGGCTGATA 600  
 548 GGGGGGACTCTGCTGCTCTTTGATAGATAGTGAAGAGGCTTTAGTGAAGAGGCTGATA 607  
 601 CAGTTTACCTAGCTGAGTGTATTTGGCTGTTCACAGCGTTTCATCTGATGGGATAGTG 660  
 608 CAGTTTACCTAGCTGAGTGTATTTGGCTGTTCACAGCGTTTCATCTGATGGGATAGTG 667  
 661 CATCGAGATCATAGGCTGAGACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGT 720  
 668 CATCGAGATCATAGGCTGAGACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGT 727  
 721 GATTTTGGATCTGCGCGGAAATGAATCAAAACAGATGGTGAATGCCAACTCCCGATT 780  
 728 GATTTTGGATCTGCGCGGAAATGAATCAAAACAGATGGTGAATGCCAACTCCCGATT 787  
 781 GGGAGCCAGATACATGCTCTCTGAGTGTGATGCTGATGATGATGATGATGATGATGAT 840  
 788 GGGAGCCAGATACATGCTCTCTGAGTGTGATGCTGATGATGATGATGATGATGATGAT 847  
 841 ACCTAGGCTGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGAT 900  
 848 ACCTAGGCTGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGAT 907  
 901 GGGAGTCCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
 908 GGGAGTCCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 967  
 961 CAGCGGTTTGTAAATTTCCAGATGACCCCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1020  
 968 CAGCGGTTTGTAAATTTCCAGATGACCCCAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1027  
 1021 CAAAGCTTGTGTGGGCGCAG 1080  
 1028 CAAAGCTTGTGTGGGCGCAG 1087  
 1081 TTCTTCTTAAATTTGACTGGAGAACCAATTCGTAACTCTCTCTCTCTCTCTCTCTCTCT 1140  
 1088 TTCTTCTTAAATTTGACTGGAGAACCAATTCGTAACTCTCTCTCTCTCTCTCTCTCTCT 1147  
 1141 CTCAGTCCGAGATGACATCTTCAATTTGATGAACCCAGAGAGAGAGAGAGAGAGAGAGAG 1200  
 1148 CTCAGTCCGAGATGACATCTTCAATTTGATGAACCCAGAGAGAGAGAGAGAGAGAGAGAG 1207  
 1201 TCCTCTCCGAGTGGAGGCTCTCAGGCTTCTCGGTTGAAGAGAGAGAGAGAGAGAGAGAG 1260  
 1208 TCCTCTCCGAGTGGAGGCTCTCAGGCTTCTCGGTTGAAGAGAGAGAGAGAGAGAGAGAG 1267  
 1261 TTTTCTAGCAGAGGAGTGGGATCTTGTGATAGTCTGTTGTGTTGTGTTGTGTTGTGTTG 1320  
 1268 TTTTCTAGCAGAGGAGTGGGATCTTGTGATAGTCTGTTGTGTTGTGTTGTGTTGTGTTG 1327  
 1321 GACTCCCTCCAGAGTGGTCCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
 1328 GACTCCCTCCAGAGTGGTCCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1387  
 1381 CAGAGCTCTCAGGAGAGGAGTGTCAAGGATTTATTTTCGAGAGGCGGCTCTCTCTCTTGC 1440  
 1388 CAGAGCTCTCAGGAGAGGAGTGTCAAGGATTTATTTTCGAGAGGCGGCTCTCTCTCTTGC 1447

QY 1441 TCCAGGATCTCTCCGCTCGGTATATATGCAAGGATCCCGCGGGCCGCTCTGCTCTGA 1500  
 DB 1448 TCCAGGATCTCTCCGCTCGGTATATATGCAAGGATCCCGCGGGCCGCTCTGCTCTGA 1507  
 QY 1501 GCGGCTGATCCGTA 1515  
 DB 1508 GCGGCTGATCCGTA 1522

RESULT 5

US-10-415-011-43  
 ; Sequence 43, Application US/10415011  
 ; Publication No. US20040053394A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION  
 ; APPLICANT: GURURAJAN, Rajagopal  
 ; APPLICANT: BAUGHN, Mariah R.  
 ; APPLICANT: CHAWLA, Narinder K.  
 ; APPLICANT: ELLIOTT, Vicki S.  
 ; APPLICANT: XU, Yuning  
 ; APPLICANT: ARVIZU, Chandra S.  
 ; APPLICANT: YAO, Monica G.  
 ; APPLICANT: RAMKUMAR, Jayalaxmi  
 ; APPLICANT: DING, Li  
 ; APPLICANT: TANG, Y. Tom  
 ; APPLICANT: HAFALIA, April J.A.  
 ; APPLICANT: NGUYEN, Dannie B.  
 ; APPLICANT: GANDHI, Ameena R.  
 ; APPLICANT: LU, Yan  
 ; APPLICANT: YUE, Henry  
 ; APPLICANT: BURFORD, Neil  
 ; APPLICANT: BANIMAN, Olga  
 ; APPLICANT: TRIBOULEY, Catherine M.  
 ; APPLICANT: LAL, Preeti G.  
 ; APPLICANT: RECEPON, Shirley A.  
 ; APPLICANT: LU, Dyung Aina M.  
 ; APPLICANT: BOBOWSKY, Mark L.  
 ; APPLICANT: THURNTON, Michael B.  
 ; APPLICANT: SWANAKER, Anita  
 ; APPLICANT: THANGAVELU, Kavitha  
 ; APPLICANT: KHAN, Farrah A.  
 ; APPLICANT: ISON, Craig H.  
 ; TITLE OF INVENTION: HUMAN KINASES  
 ; FILE REFERENCE: PI-0262 USN  
 ; CURRENT APPLICATION NUMBER: US/10/415,011  
 ; PRIOR FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: PCT/US01/47728  
 ; PRIOR FILING DATE: 2001-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/242,410  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/244,068  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/245,708  
 ; PRIOR FILING DATE: 2000-11-03  
 ; PRIOR APPLICATION NUMBER: US 60/247,672  
 ; PRIOR FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: US 60/249,565  
 ; PRIOR FILING DATE: 2000-11-16  
 ; PRIOR APPLICATION NUMBER: US 60/252,730  
 ; PRIOR FILING DATE: 2000-11-22  
 ; PRIOR APPLICATION NUMBER: US 60/250,807  
 ; PRIOR FILING DATE: 2000-12-01  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 43  
 ; LENGTH: 6298  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1  
 ; US-10-415-011-43

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361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
481 ILPSVYAKSGARGCWL 497  
481 ILPSVYAKSGARGCWL 497

RESULT 2  
US-10-238-709-2  
; Sequence 2, Application US/10238709  
; Patent No. 6680188  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-238-709-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.4e+242;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQSPSLREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQSPSLREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSFVKYSYDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
Db 61 ECSQPALMKIKHVSFVKYSYDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
Qy 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTFWIPQOYAFQDKKHLYLVNEYOPGG 180  
Db 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTFWIPQOYAFQDKKHLYLVNEYOPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Qy 241 GSAAKMNSKNVNAKLPIGTDPYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAYEMIYGR 300  
Db 241 GSAAKMNSKNVNAKLPIGTDPYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAYEMIYGR 300  
Qy 301 SPFAEGTSARTFNIMMFORLKPDPKVSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNIMMFORLKPDPKVSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
481 ILPSVYAKSGARGCWL 497  
481 ILPSVYAKSGARGCWL 497

RESULT 3

US-10-028-946-4  
; Sequence 4, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1958  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-028-946-4

Query Match 93.8%; Score 2440; DB 4; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5e+226;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQSPSLREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQSPSLREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSFVKYSYDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
Db 61 ECSQPALMKIKHVSFVKYSYDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
Qy 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTFWIPQOYAFQDKKHLYLVNEYOPGG 180  
Db 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTFWIPQOYAFQDKKHLYLVNEYOPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Qy 241 GSAAKMNSKNVNAKLPIGTDPYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAYEMIYGR 300  
Db 241 GSAAKMNSKNVNAKLPIGTDPYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAYEMIYGR 300  
Qy 301 SPFAEGTSARTFNIMMFORLKPDPKVSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNIMMFORLKPDPKVSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468

RESULT 4  
US-10-028-946-2  
; Sequence 2, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; NUMBER OF SEQ ID NOS: 4

**This Page Blank (uspto)**



**This Page Blank (uspto)**



**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 04:23:00 ; Search time 154 Seconds  
(without alignments)  
6992.501 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 9999agattgtgaagtcaaa.....tttgagcgcgtgatccgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/6C COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/6D COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515	100.0	1515	4	US-09-804-471A-1
2	1515	100.0	1515	4	US-10-238-709-1
3	1398.2	92.3	5877	4	US-10-028-946-3
4	1398.2	92.3	6165	4	US-10-028-946-1
5	963.2	63.6	2162	4	US-09-774-528-419
6	760.8	50.2	1133	4	US-09-916-204-1
7	760.8	50.2	1133	4	US-10-282-048-1
8	225.6	14.9	2726	2	US-08-422-699A-12
9	225.6	14.9	2726	2	US-08-422-706B-12
10	218.8	14.4	2511	2	US-08-422-699A-8
11	218.8	14.4	2511	2	US-08-422-706B-8
12	218.4	14.4	3182	1	US-08-484-044-11
13	216.2	14.3	17443	4	US-09-804-471A-3
14	216.2	14.3	17443	4	US-10-238-709-3
15	194	12.8	2706	2	US-08-630-822A-61
16	194	12.8	2706	2	US-09-005-069-61
17	194	12.8	2706	3	US-09-171-156A-20
18	194	12.8	2706	4	US-09-004-730A-20
19	194	12.8	2706	4	US-08-981-799A-20
20	186	12.3	4363	2	US-08-685-576-5
21	184.4	12.2	4848	4	US-09-976-594-295
22	178.8	11.8	48763	4	US-09-916-204-3
23	178.8	11.8	48763	4	US-10-282-048-3
24	175.4	11.6	4065	4	US-09-016-434-1105
25	175.4	11.6	4739	3	US-08-685-871-1
26	171.6	11.3	5053	2	US-08-685-576-2
27	156.4	10.3	3323	2	US-08-422-699A-10

28	156.4	10.3	3323	2	US-08-422-706B-10
29	125.8	8.3	3155	3	US-09-442-100-7
30	125.8	8.3	3155	4	US-08-939-106-7
31	125.8	8.3	3155	4	US-09-442-102-7
32	125.4	8.3	1498	3	US-09-509-902A-6
33	125.4	8.3	1961	3	US-09-509-902A-15
34	125.4	8.3	5276	4	US-09-233-857-2
35	121	8.0	3018	2	US-08-860-150-6
36	121	8.0	3018	3	US-09-338-132-6
37	114.6	7.6	1935	3	US-08-878-989-11
38	114.6	7.6	1935	3	US-09-272-736-11
39	113	7.5	3213	3	US-09-442-100-5
40	113	7.5	3213	4	US-08-939-106-5
41	113	7.3	1251	4	US-09-442-102-5
42	110.4	7.3	1251	4	US-09-248-796A-4400
43	108	7.1	2160	3	US-09-588-256-1
44	104.6	6.9	5720	3	US-09-442-100-1
45	104.6	6.9	5720	4	US-08-939-106-1

ALIGNMENTS

RESULT 1  
US-09-804-471A-1  
; Sequence 1, Application US/09804471A  
; Patent No. 6479269  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804.471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-471A-1

Query Match	100.0%	Score 1515;	DB 4;	Length 1515;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1515;	Conservative 0;			Gaps 0;
Qy	1	GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA	60	
Db	1	GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA	60	
Qy	61	CCCATTCGCAACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG	120	
Db	61	CCCATTCGCAACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG	120	
Qy	121	ACTCAACAGAGATGTTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTC	180	
Db	121	ACTCAACAGAGATGTTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTC	180	
Qy	181	TTTGAAGATGCACTGAGCTGCTCTGATGAAGATTAGCACTGAGCAACTTTGTCGG	240	
Db	181	TTTGAAGATGCACTGAGCTGCTCTGATGAAGATTAGCACTGAGCAACTTTGTCGG	240	
Qy	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGAGCTCGAA	300	
Db	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGAGCTCGAA	300	
Qy	301	GTCAGAGTCTTGTAGGTTGTGTCCTTTGCTGAAGTGGTGGTGAAGAGAAAGCA	360	
Db	301	GTCAGAGTCTTGTAGGTTGTGTCCTTTGCTGAAGTGGTGGTGAAGAGAAAGCA	360	
Qy	361	ACCGGGACATCTATGATGAAGTATGAGAGAGAGCTTTATTTGGCCAGGAGCAG	420	







D <sub>b</sub>	598	AAGTATTCCGACACCATAGCTGTAGTTACAGAGAGCTCCAGGCTTCAGGCAAGGACCTTCGAA	657
Q <sub>y</sub>	301	GTCCAGAAGTCTTTGTAGTGTGTGTCTCTTTGTCTGAAGTGCAGGTGTGTAAGAGAGAGAAAGCA	360
D <sub>b</sub>	658	GTCCAGAAGTCTTTGTAGTGTGTGTGTCTCTTTGTCTGAAGTGCAGGTGTGTAAGAGAGAGAAAGCA	717
Q <sub>y</sub>	361	ACGGGGACATCTATGCTATGAAAGTCACTCAAGAGAGAGGCTTTATTGGCCCGAGGACG	420
D <sub>b</sub>	718	ACGGGGACATCTATGCTATGAAAGTCACTCAAGAGAGAGGCTTTATTGGCCCGAGGACG	777
Q <sub>y</sub>	421	GTCTCATTTTTTGAGGAAGCGCGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC	480
D <sub>b</sub>	778	GTCTCATTTTTTGAGGAAGCGCGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC	837

029

838	CAATACGATATGCTTTT	CAGGACCAAAATACCTTT	ATATGCTGTCATAGGAATATCAGCTT	897
Qy	541	GGAGGGACCTTGCTGTC	CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA	600
Db	898	GGAGGGACCTTGCTGTC	CACCTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA	957
Qy	601	CAGTTTTACCTAGCTAGCTGAT	TTTGGCTGTTTCACAGCGTTTCATCTGATGGGATAGCTG	660
Db	958	CAGTTTTACCTAGCTAGCTGAT	TTTGGCTGTTTCACAGCGTTTCATCTGATGGGATAGCTG	1017
Qy	661	CATCGAGACATCAAGCCTGAGAAC	ATTCTCTGTTGACCGCACAGGACACATCAAGCTCGTG	720
Db	1018	CATCGAGACATCAAGCCTGAGAAC	ATTCTCTGTTGACCGCACAGGACACATCAAGCTCGTG	1077
Qy	721	GATTTTGGATCTGCGCGGAAAA	TGAATTCAAAACAAGTGTGTAATGCCAAACTCCCGATT	780
Db	1078	GATTTTGGATCTGCGCGGAAAA	TGAATTCAAAACAAGTGTGTAATGCCAAACTCCCGATT	1137
Qy	781	GGGACCCAGATTACATGGCT	CTCTGGAAGTGCTCACTGTGATGAACGGGGATGAAAAGGC	840
Db	1138	GGGACCCAGATTACATGGCT	CTCTGGAAGTGCTCACTGTGATGAACGGGGATGAAAAGGC	1197
Qy	841	ACCTACGGCCTGACCTGTGAT	CTGGTGGTCACTGGGCGTGATTCGCTATGAGATGATTTAT	900
Db	1198	ACCTACGGCCTGACCTGTGAT	CTGGTGGTCACTGGGCGTGATTCGCTATGAGATGATTTAT	1257
Qy	901	GGGAGATCCCCCTTCGACAGG	GAACCTCTGCGAGAACCTTCAATTAACATTAATGAATTC	960
Db	1258	GGGAGATCCCCCTTCGACAGG	GAACCTCTGCGAGAACCTTCAATTAACATTAATGAATTC	1317
Qy	961	CAGCGGTT	968	
Db	1318	CAGGTGTT	1325	

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RESULT 6
US-09-916-204-1
; Sequence 1, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Human
US-09-916-204-1
Query Match          50.2%; Score 760.8; DB 4; Length 1133;
Best Local Similarity 99.7%; Pred. No. 1.4e-244;

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Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 60
DB 48 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 107
QY 61 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 120
DB 108 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 167
QY 121 ACTCAACAGCAGATGCTCTCTCTCTCCAGAGAGGATATTAAGTCCCTCTTTGTTCTC 180
DB 168 ACTCAACAGCAGATGCTCTCTCTCTCCAGAGAGGATATTAAGTCCCTCTTTGTTCTC 227
QY 181 TTTGAAGATGAGTCAAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 240
DB 228 TTTGAAGATGAGTCAAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 287
QY 241 AAGTATTCGACACCATAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 300
DB 288 AAGTATTCGACACCATAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 347
QY 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAAGTCAAGTCAAGTCAAGTCAAGT 360
DB 348 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAAGTCAAGTCAAGTCAAGTCAAGT 407
QY 361 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
DB 408 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 467
QY 421 GTTTCATTTTTCGAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCTGATCC 480
DB 468 GTTTCATTTTTCGAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCTGATCC 527
QY 481 CAATTACAGTATGCTCTTTCAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCT 540
DB 528 CAATTACAGTATGCTCTTTCAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCT 587
QY 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGAGCGGAAACATATTTATCT 600
DB 588 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGAGCGGAAACATATTTATCT 647
QY 601 CAGTTTACCTAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 648 CAGTTTACCTAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
QY 661 CATCGAGACATCAAGCTTGAAGCATTCTGTTGACCGCAGGACACATCAAGCTGGTG 720
DB 708 CATCGAGACATCAAGCTTGAAGCATTCTGTTGACCGCAGGACACATCAAGCTGGTG 767
QY 721 GATTTTGGATCTCCCGGAAATGAATTCAAAACAGATGGTAA 764
DB 768 GATTTTGGATCTCCCGGAAATGAATTCAAAACAGATGGTAA 811

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RESULT 7
US-10-282-048-1
; Sequence 1, Application US/10282048
; Patent No. 692948
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Human

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US-10-282-048-1
Query Match 50.2%; Score 760.8; DB 4; Length 1133;
Best Local Similarity 99.7%; Pred. No. 1.4e-244;
Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 60
DB 48 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 107
QY 61 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 120
DB 108 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 167
QY 121 ACTCAACAGCAGATGCTCTCTCTCTCCAGAGAGGATATTAAGTCCCTCTTTGTTCTC 180
DB 168 ACTCAACAGCAGATGCTCTCTCTCTCCAGAGAGGATATTAAGTCCCTCTTTGTTCTC 227
QY 181 TTTGAAGATGAGTCAAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 240
DB 228 TTTGAAGATGAGTCAAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 287
QY 241 AAGTATTCGACACCATAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 300
DB 288 AAGTATTCGACACCATAGTCTGATGAAGATTAAGCAGTCAAGTCAAGTCAAGTCAAGT 347
QY 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAAGTCAAGTCAAGTCAAGTCAAGT 360
DB 348 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAAGTCAAGTCAAGTCAAGTCAAGT 407
QY 361 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
DB 408 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 467
QY 421 GTTTCATTTTTCGAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCTGATCC 480
DB 468 GTTTCATTTTTCGAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCTGATCC 527
QY 481 CAATTACAGTATGCTCTTTCAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCT 540
DB 528 CAATTACAGTATGCTCTTTCAGGAGCGGAAACATATTTATCTCGAAGCACAAGCCGCT 587
QY 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGAGCGGAAACATATTTATCT 600
DB 588 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGAGCGGAAACATATTTATCT 647
QY 601 CAGTTTACCTAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 648 CAGTTTACCTAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
QY 661 CATCGAGACATCAAGCTTGAAGCATTCTGTTGACCGCAGGACACATCAAGCTGGTG 720
DB 708 CATCGAGACATCAAGCTTGAAGCATTCTGTTGACCGCAGGACACATCAAGCTGGTG 767
QY 721 GATTTTGGATCTCCCGGAAATGAATTCAAAACAGATGGTAA 764
DB 768 GATTTTGGATCTCCCGGAAATGAATTCAAAACAGATGGTAA 811

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RESULT 8
US-08-422-699A-12
; Sequence 12, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```



ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02713

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/422,699A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/422,706

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/023,612

FILING DATE: 26-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/839,255

FILING DATE: 20-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/01545

FILING DATE: 19-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00253

FILING DATE: 05-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB9202485.0

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5830A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2726 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-422-699A-12

Query Match 14.9%; Score 225.6; DB 2; Length 2726;

Best Local Similarity 54.0%; Pred. No. 1.3e-64;

Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;

QY 200 CTGCTCTGATGAAGATTACGAGTGGAGCACTTTGTCGGAGATATTCGGACACCATAG 259  
 Db 243 CCGAACTGGCCGAGGACAGTACGTGGCGGACTTCTTGAGGTGGGGAGCCCATCGTG 302  
 QY 260 CTGAGTTACAGGAGCTCCAGCCCTCGGCAAGACTTCGAAGTTCAGAACTTTGAGGTT 319  
 Db 303 TGAGGCTTAAGAGGTCCGACTCTCAGAGGAGCACTTCAGATCTGAAGGTGATCGGAC 362  
 QY 320 GTGGTCACTTTGCTGAAGTCCAGGTGGTAAGAGAGAAACACCGGGGACATCTATGCTA 379  
 Db 363 GCGGGGCGTTTCAGGAGGTAGCGGTAGTGAAGATGAAGCAGACGGGCCAGGTGTATGCCA 422  
 QY 380 TGAAGTGAAGAGAGAGGCTTTATGCGCCAGGAGGAGGTTTCATTTTGTAGGAG 439  
 Db 423 TGAAGTGAAGAGAGGCTTTATGCGCCAGGAGGAGGTTTCATTTTGTAGGAG 482  
 QY 440 AGCGGAGCACTTATCTCGAAGCAGCAAGCCCGGTGGATCCCCCAATTTACAGTATGCTTTTC 499  
 Db 483 AGAGGAGCGTTGTTGATGATGGGACCGCGGTGGATCAGCAGCTGCATCTCGCTTCC 542  
 QY 500 AGGACAAAAATCACCTTTATCTGTCATGAATATCAGCTGGAGGGGACTTCTGCTCAC 559

Db 543 AGGATGAGAACTACCTGTACCTGTGCTGATGAGTATTACGTGGGGGAGACCTGCTGACAC 602  
 QY 560 TTTTGAATAGATATGAGGACCACTTAGTGAACCTGATACAGTTTACCTAGCTGAGC 619  
 Db 603 TGCTGAGCAAGTTTGGGAGCGGATTCCGGCCGAGATGGCGGCTTTACCTGCGGAGA 662  
 QY 620 TGATTTTGGCTGTTTACAGACCTTCTATCTGATGGGATACCTCATCGAGACATCAAGCTG 679  
 Db 663 TTGTCATGGCCATAGACTCGGTGACCGGCTTGGCTAGTGCACAGGAGACATCAACCG 722  
 QY 680 AGAACATTTCTGTTGACCGGACAGACACATCAAGCTGGTGGATTTTGGATCTCCCGGA 739  
 Db 723 ACAACATCTCTGTCGACCGCTGTGGCCACATCCCGCTGGCGGACTTGGCTCTTGCCTCA 782  
 QY 740 AAATGAATTTCAACAAAGATGTTGAATGCCAAATCCCGATTGGGACCCAGATACATG 799  
 Db 783 AGTGGGGGAGATGGAACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 842  
 QY 800 CTCCTGAAGTCTGA---CTGTGATGAACGGGGATGGAAGAGCACTTACCGCTTGGACT 856  
 Db 843 CCCCCGAGATCTTCAGGCTGTGGCGGTGGGCTGGGACAGGAGCTTACCGGCGCGAGT 902  
 QY 857 GTGACTGGTGTGCTGAGTGGGCTGATTCCTATGATGATGATTTATGGGAGATCCCGCTTCG 916  
 Db 903 GTGACTGGTGGGCTGGGTGATTCGCTATGAATGTTCTATGGGAGACGCGCTTCT 962  
 QY 917 CAGAGGGAACCTCTGCCAGAACCTTCAATTAACATTATGAATTTCCAGCGGTTTTTGAAT 976  
 Db 963 ACGCGGATTTCCACGGGAGAGCTTATGCAAGATCGTCCACTACAAGAGCACCTCTCTC 1022  
 QY 977 TTCCAGATGACCCCAAGTGAAGT---GACTTTCTGATCTGATTTCAAGCTTGTGT 1033  
 Db 1023 TGCCGCTGGTGGAGGAGGCTTCCCTGAGGAGGCTCGAGACTTCAATTCAGCGGTGCTGT 1082  
 QY 1034 GCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGC-----CATCCTTTCT 1084  
 Db 1083 GTCCCCCGAGACACGCTGGCGGGGTGGAGAGGAGCTTCCGGACACATCCCTTCT 1142  
 QY 1085 TCTCTAAATTTGACTGGAACAACTTCGTAACCTCTCTCCCGCTTCTGTTCCCAACCTCA 1144  
 Db 1143 TCTTTGGCTCGACTGGGATGCTCTCGGGAGACGCTGCGCCCTTTTACACCGGATTCG 1202  
 QY 1145 AGTCCGAGATGACACCTCCAAATTTGA 1172  
 Db 1203 AAGTGCCACCGACATGCAACTTCA 1230

# RESULT 9

US-08-422-706B-12

Sequence 12, Application US/08422706B

Patent No. 5977333

GENERAL INFORMATION:

APPLICANT: Brook, J. David

APPLICANT: Housman, David E.

APPLICANT: Shaw, Duncan J.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Keith J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02713

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/422,706B  
 / FILING DATE: 14-APR-1995  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA: US 08/284,543  
 / APPLICATION NUMBER:  
 / FILING DATE: 08-AUG-1994  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/023,612  
 / FILING DATE: 26-FEB-1993  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 07/839,255  
 / FILING DATE: 20-FEB-1992  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: PCT/US93/01545  
 / FILING DATE: 19-FEB-1993  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: PCT/GB93/00253  
 / FILING DATE: 05-FEB-1993  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: GB9202485.0  
 / FILING DATE: 06-FEB-1992  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Granahan, Patricia  
 / REGISTRATION NUMBER: 32,227  
 / REFERENCE/DOCKET NUMBER: MIT-5830A2  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 617-861-6240  
 / TELEFAX: 617-861-9540  
 / INFORMATION FOR SEQ ID NO: 12:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 2726 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: double  
 / TOPOLOGY: linear  
 / US-08-422-706B-12

Query Match 14.9%; Score 225.6; DB 2; Length 2726;  
 Best Local Similarity 54.0%; Pred No. 1.3e-64;  
 Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;  
 QY 200 CTGCTCTGATGAAGATTAAAGCAGTGGAGCAACTTTTTCGGGAAGTATTCGACACCACTAG 259  
 Db 243 CCGAACTGCCAGGACAGTACGTGGCGCACTTTCTTGCAGTGGCGGAGCCCATCGTGG 302  
 QY 260 CTGAGTTACAGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAGTCTGTAGATT 319  
 Db 303 TGAGGCTTAAGAGGTCCGACTGCGAGGGAGCACTTCGAGANTCTGAAGTGTATCGGAC 362  
 QY 320 GTGGTCACTTTGCTGAAGTGCAGGTGGTAAAGAGAAAGCAACCGGGGACATCTATGCTA 379  
 Db 363 CGGGGCGGTTACGAGGTAGCGGTAGTGAAGATGAAGCAGACGGGCCAGGTGTATGCCA 422  
 QY 380 TGAAGTGTAGAGAGAAAGCTTTTATGGCCAGCAGCAGGTTTCATTTTGGAGGAG 439  
 Db 423 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGCGGAGGTGCTGCTTCGCTGAGG 482  
 QY 440 AGCGGAACATATTAATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCTTTC 499  
 Db 483 AGAGGACGTTGTTGATGAGGAGCGGCGGTGATCAGCAGCTGCACCTTCGCTTC 542  
 QY 500 AGGACAAAATCACCTTTATCTGTCATGGAATATCAGCTGGAGGAGCACTTGTGTGAC 559  
 Db 543 AGGATGAGAACTACCTGTACCTGGTTCATGGAGTATTAGTGGCGGGGACCTGTGTGAC 602  
 QY 560 TTTTGAATAGATATGAGGACCACTAGATGAAGAACTGATACAGTTTTACCTAGCTAGC 619  
 Db 603 TCTGAGCAGTTTGGGAGCGGATTCGGCCGAGATGGCGGCTTCTACCTGGCGGAGA 662  
 QY 620 TGATTTGGCTTTTCAAGCGGTTCACTGATGGGATACGTGATGAGACATCAAGCGT 679  
 Db 663 TTGTATGCCCATAGACTCGGTGCAACCGGCTTGGCTAGGTGACAGAGGACATCAAAACCG 722

QY 680 AGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGCGCA 739  
 Db 723 ACAACATCTCTGTTGACCGCTGTGGCCACATCCGCTGGCCGACTTTCGCTCTGCTCA 782  
 QY 740 AATGAATTCAAACAGATGGTGAATGCCAAATCCGATTCGGATTCGGACCCAGATATATGG 799  
 Db 783 AGCTGCGGCGAGATGGAACGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842  
 QY 800 CTCCTGAAGTGTCTGA---CTGTGATGAAGCGGGATGAAAAAGGCACCTACGGCTCGACT 856  
 Db 843 CCCCAGATCTCTGAGGCTGTGGCGGTGGGCTTGGACAGGACGCTACGGGCGCGAGT 902  
 QY 857 GTGACTGCTGCTGAGTGGCGGTGATTCCTATGAGATGATTTATGGAGATCCCCCTTGG 916  
 Db 903 GTGACTGCTGCTGAGTGGCGGTGATTCCTATGAGATGATTTATGGAGATCCCCCTTGG 962  
 QY 917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 976  
 Db 963 ACGGGATTCACGGCGGAGACCTATGGCAAGATCGTCACTACAAGGAGCAGCTCTCTC 1022  
 QY 977 TTCAGATGACCCCAAGTGGAGCAGT---GACTTTCTTGTATCTGATTCGATTCGATTCGAT 1033  
 Db 1023 TGGCGCTGTGGAGCAAGGGTCTCTGAGGAGGCTCGAGACTTCATTACGCGGTTGCTCT 1082  
 QY 1034 CGGCGCAGAGAGAGAGACTGAAGCTTTGAAGGCTTTTGGCTGC-----CATCTTTCT 1084  
 Db 1083 GTCCCCGGAGACACCGCTGGCGGGGTGGAGCAGGCACTTCGCGACACATCCCTTCT 1142  
 QY 1085 TCTTAAATTTGATGGAACAACATTCGTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1144  
 Db 1143 TCTTTGCGCTCGACTGGGATGGTCTCCGGGACAGCGTGCCCGCTTTTACACGGAATTCG 1202  
 QY 1145 AGTCCGACGATGACACTCCAAATTTGA 1172  
 Db 1203 AAGGTCCACCGACACATGCAACTCGA 1230

RESULT 10  
 US-08-422-699A-8  
 ; Sequence 8, Application US/08422699A  
 ; Patent No. 5955265  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brook, J. David  
 ; APPLICANT: Housman, David E.  
 ; APPLICANT: Shaw, Duncan J.  
 ; APPLICANT: Harley, Helen G.  
 ; APPLICANT: Johnson, Keith J.  
 ; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC  
 ; DYSTROPHY GENE AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 ; STREET: Two Militia Drive  
 ; CITY: Lexington  
 ; STATE: Massachusetts  
 ; COUNTRY: US  
 ; ZIP: 02713  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/422,699A  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/422,706  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/023,612  
 ; FILING DATE: 26-FEB-1993  
 ; PRIOR APPLICATION DATA:



APPLICATION NUMBER:	US 07/839,255
FILING DATE:	20-FEB-1992
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	PCT/US93/01545
FILING DATE:	19-FEB-1993
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	PCT/GB93/00253
FILING DATE:	05-FEB-1993
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	GB9202485.0
FILING DATE:	06-FEB-1992
ATTORNEY/AGENT INFORMATION:	
NAME:	Granahan, Patricia
REGISTRATION NUMBER:	32,227
REFERENCE/DOCKET NUMBER:	MIT-5830A2
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	617-861-6240
TELEFAX:	617-861-9540
INFORMATION FOR SEQ ID NO:	8:
SEQUENCE CHARACTERISTICS:	
LENGTH:	2511 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	double
TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)
FEATURE:	
NAME/KEY:	CDS
LOCATION:	1..1746
US-08-422-699A-8	

  

Query Match	14.4%;	Score 218.8;	DB 2;	Length 2511;
Best Local Similarity	54.5%;	Pred. No. 2.4e-62;		
Matches 511;	Conservative 0;	Mismatches 412;	Indels 15;	Gaps 3;

  

QY	250	GACACCATAGCTGAGTTACAGAGCTCCAGCCTTCGCCAAGGACTTCGAACTCAGAAGT	309
DB	43	GCACCTCGTGGTGAAGGCTTCGAGAGGACACTTCGAGATTCTGAAG	102
QY	310	CTTTAGGTTGTGGTCACTTTTGCTGAAGTGCAGGTGTAAGAGAGAAACCAACCGGGAC	369
DB	103	GTGATCGACGCGGGCGCTTCAGCGAGTAGCGGTAGTAAGATGAAGACAGCGGCCAG	162
QY	370	ATCTATGCTATGAAGTGAAGAAAGAGCTTTATTGGCCCAAGAGAGAGGTTTCATT	429
DB	163	GTGTATGCCATGAAGATCATCAACAAGTGGGACATGCTGAAGAGGGCGAGGTGCTGC	222
QY	430	TTTGAGGAAGACGGAACATATATCTCGAAGCACAGCCCTGGATCCCCAATTACAG	489
DB	223	TTCCGTGAGGAGGGGACGTGTTGGTAATGGGACCGGCGGTGGATCAGCAGCTGCAC	282
QY	490	TATGCTTTTCAGGACAAAATCACCTTTATCTGGTCAATGAATATCAGCCTCGAGGGGAC	549
DB	283	TTCCGCTCCAGGATGAGAACTACTCTGTACTGGTCAATGAGTATTACGTGGCGGGAC	342
QY	550	TTGCTGTCACTTTTGAATAGATATGAGGACAGTTAGATGAACCTGATACAGTTTAC	609
DB	343	CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGATCCGCCCGAGATGGCGCGCTTCTAC	402
QY	610	CTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTGATCGAGAC	669
DB	403	CTGGCGGAGATTGTCAATGCCATAGACTCGGTGCACCGGCTTGGCTACGTGCACAGGAC	462
QY	670	ATCAGCCTGAGAACTTCTGTTGACCGCAGGACACATCAGCTGGTGGATTTTGA	729
DB	463	ATCAAAACCGACAACTCTGCTGACCGCTGTGGCCACATCCGCTTGGCGGACTTCGGC	522
QY	730	TTTCCCGGAAAAATGAATTCAAAACAAGATGGTGAATGCCAAATCTCCCGATTGGGACCCCA	789
DB	523	TCTTGCTCAAGCTCGGGCAGATGGAACGTTGGGTGCTGTTGGTGTGGGACCCCA	582
QY	790	GATTACATGGCTCTCGA---AGTGTGATCTGTGATGAACGGGATAGAAAAGGCACTTAC	846
DB	583	GACTACTCTCCCGGAGATCTCGAGGCTTGGCGGCTGGGCTGGGACAGCAGCTAC	642

ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5830A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2511 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1746  
US-08-422-706B-8

Query Match 14.4%; Score 218.8; DB 2; Length 2511;  
Best Local Similarity 54.5%; Pred. No. 2.4e-62;  
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;

QY 250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCCTTCGGCAAGGACTTCGAAGTCAGAGT 309  
Db 43 GCATCGTGTGAGGCTTAAGGAGGTCGAGCTGCAGAGGAGACTTCGAGATTCTGAAG 102  
QY 310 CTTGTAGGTTGTGGTCACTTTGCTGAAGTCAGGTTGTAAGAGAGAAACCAACCGGGGAC 369  
Db 103 GTGATCGGACGGGGCGTTTCAGCAGGTTAGCGGTAGTGAAGATGAAGCAGAGCGGCCAG 162  
QY 370 ATCTATGCTATGAAGTATGAAGAAGAGGCTTTATGCGCCAGGAGGAGGTTTCATTT 429  
Db 163 GTGATGCTATGAAGTATGAAGAAGTGGGACATGCTGAAGAGGGGGGAGGTGTCGTGC 222  
QY 430 TTTGAGGAGAGCGGAACTATTATCTCAAGCACAAGCCGCTGGATCCCCCAATACAG 489  
Db 223 TTCCGTTGAGGAGGAGCGCTGTTGTTGATGGGACCGCGGTGGATCAGGAGCTGCAC 282  
QY 490 TATGCTTTTCAGAGCAAAATACCTTTTATCTGGTATGGAATATCAGCCTGGAGGGGAC 549  
Db 283 TTGCGCTTCAGGATGAGAACTACCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 342  
QY 550 TTCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGTGAACCTGATACAGTTTAC 609  
Db 343 CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGCGCCGAGATGCGCGCTTCTAC 402  
QY 610 CTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTTCACTGATGGGATAGCTGATCGAGAC 669  
Db 403 CTGGCGGAGATTGCTATGCGCCATAGACTCGGTGACCGGCTTTGGTACGTGACAGGAG 462  
QY 670 ATCAAGCTGAGAGACTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTTGA 729  
Db 463 ATCAAAACCGCAACATCTCTGTCGACCGCTGTGGCCACATCCGCTGGCGGAGTTCGCG 522  
QY 730 TCTGCGCGAAATGAATTAACAAGATGTTGAATGTCGCAACTCCCGATTGGGACCCCA 789  
Db 523 TCTTGCTCAAGCTGGGCGGACATGAAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582  
QY 790 GATTACATGGCTCTGA---AGTGTGATGATGATGAAGCGGGATGGAAGAGGACCTAC 846  
Db 583 GACTACTGTCCTCCCGAGATCTCTGAGGCTGTGGGCGGTGGGCGCTGGGACAGGAGCTAC 642  
QY 847 GGCTGAGCTGACTGGTGGTGGTGGGCGGATGCTGATGATGATGATGATGATGATGATGATGAT 906  
Db 643 GGGCCCGAGTGTGACTGGTGGGCGGTGGGCTGATGCTGATGATGATGATGATGATGATGATGAT 702  
QY 907 TCCCTCTTCGAGAGGGAACCTCTGTCAGAAACCTTCAATATCAATATGAATTTTCAGGGG 966  
Db 703 AGCGCTTCTACCGGATTTCCACGGCGGAGAGCTATGGCAAGATCGTCACTTCAAGAGG 762  
QY 967 TTTTGAATTTCCAGATGACCCCAAGATGAGCAGT---GACTTTCTTGTATCTGATTCAA 1023

Db 763 CACCTCTCTGCGCTGGTGGAGGAAGGGTCCCTGAGGAGGCTCGAGACTTCATTACAG 822  
QY 1024 AGCTTGTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTTTGTCTGCTG 1074  
Db 823 CGGTTGCTGTGTCCCGGAGACACCGCTGGCGGGTGGAGCGGAGCTTCCGAGACA 882  
QY 1075 CATCTTTCTCTCTAAATTTGACTGGAAACAACATTCGTAACCTCTCTCCCTCCCTTCGTT 1134  
Db 883 CATCCCTCTCTTTTGGCTCGACTGGATGGTCTCGGGACAGCGTGGCGCTTTTACA 942  
QY 1135 CCCACCTCAAGTCCGAGATGACACCTCCAAATTTGA 1172  
Db 943 CCGGATTTGGAAGGTGCCCGGACACATGCAACTTCGA 980

RESULT 12  
US-08-484-044-11  
; Sequence 11, Application US/08484044  
; Patent No. 5552282  
; GENERAL INFORMATION:  
; APPLICANT: Caskey, C. T.  
; APPLICANT: Fu, Ying-Hui  
; APPLICANT: Friedman, David L.  
; APPLICANT: Pizzuti, Antonio  
; APPLICANT: Fenwick, Raymond G.  
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski, L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,044  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/019,940  
; FILING DATE: 19-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5443  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-484-044-11

Query Match 14.4%; Score 218.4; DB 1; Length 3182;  
Best Local Similarity 54.5%; Pred. No. 3.8e-62;  
Matches 510; Conservative 0; Mismatches 411; Indels 15; Gaps 3;

QY 252 CACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCAAGGACTTCGAAAGTCAGAGTCT 311  
Db 743 CATCGTGTGAGGCTTAAGGAGGTCGCTGAGAGGGGAGGAGCTTCGAGATTCTGAAGT 802  
QY 312 TGATGTTGTTGTCATTTGCTGAGTGCAGGTGGTAAAGAGAGAAAGCAACCGGGACAT 371

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Db 803 GATCGGACGCGGGCGTTCAGCGAGGTAGCGGTAGTGAAGATGAACAGACGCGGCACGGT 862
Qy 372 CTATGCTATCAAGATGATGAAGAGAGGCTTTATTGGCCCGCAGGACAGGTTTCATTTT 431
Db 863 GTATGCCATGAAGTATGATGAAGTGGGACATGCTGAAGAGGGGCGAGGTGCTGCTT 922
Qy 432 TGAGGAGAGCGGAAATATATCTCGAAGCAAGCCCGTGTGATCCCGAATACAGTA 491
Db 923 CCGTGAGGAGAGGAGCGGTGTGTGTAATGGGACCGCGCGGTGGATCACGCGAGTGCAC 982
Qy 492 TGCCTTTCCAGACAAATACCTTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTT 551
Db 983 CGCCTTCCAGATGAGAGACTACCTGTACCTGTGTCATGGAGTATACGTGGCGGGACCT 1042
Qy 552 GCTGTACTTTTGAATAGATATGAGGACCAAGTATGATGAAGAACTGATACAGTTTACCT 611
Db 1043 GCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGCGCGAGATGGCGGCTTACCT 1102
Qy 612 AGCTGAGCTGATTTTGGCTGTTACAGCGTTCATCTGATGGGATAGTGCATCGACAT 671
Db 1103 GCGGAGATTTGATGGCCATAGACTCGGTGACCGGCTTGGCTAGTGTGCACAGGACAT 1162
Qy 672 CAAGCTTGAGAAATCTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATC 731
Db 1163 CAAGCCGACAAATCTCTGTTGACCGCTGTGCGCACATCCGCTGGCGGACTTGGCTC 1222
Qy 732 TGC CGCAAAATGAAATCAACAGATGTTGAATGCCAACTCCGATTTGGGACCCAGA 791
Db 1223 TTGCTCAAGCTCGGCGACATGAACCGGTGCGGTGCTGCTGGTGGCTGCGGACCCAGA 1282
Qy 792 TTACATGGCTCCTGA---AGTGTGACTGTGATGAACCGGGATGGAAGGACACCTACCG 848
Db 1283 CTACTCTCCCGAGATCTCGCAGGCTGTGGCGGTGGCTGGACAGGACGCTACGG 1342
Qy 849 CTGGAATGACTGTGTTGCTGAGTGGCGGTGATGCTGATGATGATGATTTATCGGAGATC 908
Db 1343 GCGGAGTGTGACTGTGGCGGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1402
Qy 909 CCGCTTCGAGAGGAGACTCTCCAGAACCTTCAATACATTAATGATTTTCAGCGGTT 968
Db 1403 GCCCTTTCAGGATTTCCAGCGGAGACTATGGAGAGATGCTCCATACAGAGCA 1462
Qy 969 TTTGAAATTTCCAGATACCCCAAGATGAGCAGT---GACTTTCTGATCTGATCAAA 1025
Db 1463 CCTCTCTGCGCTGTGGACGAAGGGTCCCTGAGGAGCTCGAGACTTCATTTCAGCG 1522
Qy 1026 CTTGTTGCGGCGCAGAGAGACTGAAGTTTGAAGTTTGAAGTTTGTGCTG-----CA 1076
Db 1523 GTTGCTGTGCTCCCGGAGACACGCTGGGCGGGGTGGAGCGGAGCTTCCGAGACAC 1582
Qy 1077 TCCTTTCTTCTCTAAAATTGACTGGAACAACTTCGTAATCTCTCCCTCCCGCTTCGTTCC 1136
Db 1583 TCCCTTCTTCTTGGCCTCGACTGGGATGGTCTCGGAGACAGCGTGGCCCTTTACACC 1642
Qy 1137 CACCTCAAGTCGACGATGACACTCCAAATTTGA 1172
Db 1643 GGATTTGGAAGGTCCACCGACACATGCAACTTGA 1678

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RESULT 13
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match 14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 3.5e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1287 TCTTGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGTCCAT 1346
Db 171282 TTTTCTCTACCTAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGTCCAT 171341
Qy 1347 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAA 1406
Db 171342 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAA 171401
Qy 1407 GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCGTCGGTATATGC 1466
Db 171402 GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCGTCGGTATATGC 171461
Qy 1467 CAAGGGATCCGCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 1515
Db 171462 CAAGGGATCCGCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 171510

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RESULT 14
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

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Query Match 14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 3.5e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1287 TCTTGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGTCCAT 1346
Db 171282 TTTTCTCTACCTAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGTCCAT 171341
Qy 1347 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAA 1406
Db 171342 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAA 171401
Qy 1407 GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCGTCGGTATATGC 1466
Db 171402 GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCGTCGGTATATGC 171461
Qy 1467 CAAGGGATCCGCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 1515

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Db 171462 CAAGGATCCCGCGGCGCGCTGCTGCTCTGAGCGCGCTGATCGTA 171510

## RESULT 15

US-08-630-822A-61  
 ; Sequence 61, Application US/08630822A  
 ; Patent No. 5840695  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANK, GLENN R.  
 ; APPLICANT: HUNTER, SHIRLEY WU  
 ; APPLICANT: WALLENFELS, LYNDIA  
 ; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
 ; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,822A  
 ; FILING DATE: 11-APR-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CONNELL, GARY J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2618-17-C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 61:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2706 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 5..2706

US-08-630-822A-61

Query Match 12.8%; Score 194; DB 2; Length 2706;  
 Best Local Similarity 54.4%; Pred.No. 5.3e-54;  
 Matches 492; Conservative 0; Mismatches 385; Indels 27; Gaps 4;  
 QY 287 CAAAGGACTCGAAGTCAGAAGCTTTGTAGGTGTGGTCACCTTTGCTGAAGTCGAGGTGG 346  
 DB 78 CAGATGATTTTAATTAATAAAGTTATTGGTCGAGGACATTTGGTGAAGTACAGTTAG 137  
 QY 347 TAAGAGAGAAAGCAACCGGGACATCTATGCTATGAAGTGATGAAGAGAGGCTTTAT 406  
 DB 138 TCGCACACAAATCAACTGCACAAAGTTTGTCTATGAAGCGCTATCAAAATTTGAAATGA 197  
 QY 407 TGGCCCGAGGAGGAGTTTCATTTTGTAGGAAGAGCGGAACATATATCTCGAAGCAAA 466  
 DB 198 TTAAGAGACGACAGCTCTGATTTTGTGGAGAACGTCATATATGCTCATGCAAAAT 257  
 QY 467 GCCCGTGGATCCCGAATTTACAGTAGCTTTTACAGACAAAAATCACCTTTTATCTGGTCA 526  
 DB 258 CAGATGGATTTGACAAATTTACATTTTGTCTTTTCAAGATCAAAATATCTTTATATGGTCA 317  
 QY 527 TGGAAATATCAGCTCGAGGGGACTTGTCTGCTACTTTTGAATAGATATGAGGACCAAGTTAG 586  
 DB 318 TGGATTATATCGCGGGGGTGACTTGGTGAGTCTTAGT-----TCCGATTATGAATTC 371

QY 587 ATGAAACCTGATACAGATTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTTCATC 646  
 DB 372 CAGAAAATATGGGCAATGTTCTTATACAATGGAAGTGGTGCTAGCACTTTGATACAAATTCAC 431  
 QY 647 TGATGGGATACGTGATCGAGACATCAAGCTCTGAGAACATTTCTCGTTTGACCGCACAGGAC 706  
 DB 432 CCATGGGATTTGTATACATCGTGATGTTAAACCTGATATATATGCTTCTAGACAAATATGTC 491  
 QY 707 ACATCAAGCTGCTGATTTTGGATCTCGCGGAAAATGAATTCAAAACAGATGCTGAATG 766  
 DB 492 ATTTAAAGTTAGCTGACTTTTGGAACTCTGTATGAAAATGATACAGATGTTTGGTAGTT 551  
 QY 767 CCAAACTCCCGATTGGGACCCCGACGATTACATGCTCTGAAAGTCTGACTGTGATGAACG 826  
 DB 552 CTATATATGCTGTGGAAACGCTGATTACATTTCTCCGAGT-----TTTGCAGTCCC 605  
 QY 827 GGGATGGAAGGACCTAGCGCTGAGCTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886  
 DB 606 AAGGTGGTGAAGGAGTTTACCGTCTGTAATCGGATTCGATTCGCTGCTGCTGCTGCTGCT 665  
 QY 887 ATGAGATGATTTATGGGAGATCCCTCTTCGAGAGGGAACCTCTGCCAGAACCTTCAATA 946  
 DB 666 ATGAAATGTTATTTGGAGAACACCTTTTATGACAGACAGTTCGTTGGTGGAACTTACAGTA 725  
 QY 947 ACATTATGAATTTCCAGCGGTTTTTGAATTTCCAGATGACCCCAAGAGTGAGCAGTGACT 1006  
 DB 726 AAATTATGGATCACAGAAACTCATTAACCTTTCTCCAGAAAGTGAATAAAGCCAATATG 785  
 QY 1007 TTCTTGATCTGATTCAGAAAGCTTGTGTCGCGCCAGAAAG-----AGACTGAAGT 1057  
 DB 786 CCCGATCTTTGATACAAAGATTTTAAACAGACAGAACACAGCGCTTTAGGCAGAAATGAAG 845  
 QY 1058 TTGAAGGTCTTTGCTGCCATCCTTTCTCTCTAAAATTTGACTGGA-----ACAACATTC 1111  
 DB 846 TGAAGAAGAAATTAACAGACATCCATTTTTCATAAATGATCAATGAGCTTTTGGACAAATTA 905  
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 DB 906 GAGACTCTGCCCACTCTGATGCTGAGCTGAGCTGAGCTGATGATGATGATGATGATGATG 965  
 QY 1172 ATGA 1175  
 DB 966 ATGA 969

Search completed: November 8, 2004, 08:55:10  
 Job time : 159 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 12:23:11 ; Search time 39 Seconds

(without alignments)  
845.129 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFYKARNPLDAGAAEPI.....CSRILSVYAKSGARGCWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*\*  
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2: /cgm2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	497	4	US-09-804-471A-2
2	2602	100.0	497	4	US-10-238-709-2
3	2440	93.8	1958	4	US-10-028-946-4
4	2440	93.8	2054	4	US-10-028-946-2
5	2271.5	87.3	494	4	US-09-804-471A-4
6	2271.5	87.3	494	4	US-10-238-709-4
7	1284	49.3	257	4	US-09-916-204-2
8	1284	49.3	257	4	US-10-282-048-2
9	1180	45.3	251	4	US-09-916-204-4
10	1180	45.3	251	4	US-10-282-048-4
11	1177	45.2	251	4	US-09-916-204-5
12	1177	45.2	251	4	US-09-916-204-6
13	1177	45.2	251	4	US-10-282-048-5
14	1177	45.2	251	4	US-10-282-048-6
15	865	33.2	1388	4	US-08-685-576-4
16	865	33.2	1388	4	US-09-976-594-296
17	864.5	33.2	1354	3	US-08-685-871-2
18	860.5	33.1	1388	2	US-08-685-576-1
19	857.5	33.0	420	3	US-08-685-871-58
20	840.5	32.3	420	3	US-08-685-871-59
21	828	31.8	582	2	US-08-422-699A-9
22	828	31.8	582	2	US-08-422-706B-9
23	790.5	30.4	900	2	US-08-630-822A-62
24	790.5	30.4	900	2	US-09-005-069-62
25	790.5	30.4	900	3	US-08-171-156A-21
26	790.5	30.4	900	4	US-09-004-730A-21
27	790.5	30.4	900	4	US-08-981-799A-21

28 771.5 29.7 638 2 US-08-422-699A-11 Sequence 11, Appl  
29 771.5 29.7 638 2 US-08-422-706B-11 Sequence 11, Appl  
30 760.5 29.2 555 1 US-08-484-044-6 Sequence 6, Appl  
31 711 27.3 479 3 US-09-442-100-13 Sequence 13, Appl  
32 711 27.3 479 4 US-08-939-106-13 Sequence 13, Appl  
33 711 27.3 479 4 US-09-442-102-13 Sequence 13, Appl  
34 701 26.9 526 3 US-09-442-100-12 Sequence 12, Appl  
35 701 26.9 526 4 US-08-939-106-12 Sequence 12, Appl  
36 701 26.9 526 4 US-09-442-102-12 Sequence 12, Appl  
37 686 26.4 719 3 US-09-588-256-2 Sequence 2, Appl  
38 683 26.2 404 2 US-08-860-150-3 Sequence 3, Appl  
39 683 26.2 404 3 US-09-338-132-3 Sequence 3, Appl  
40 677 26.0 464 2 US-08-878-989-4 Sequence 4, Appl  
41 677 26.0 464 3 US-09-272-796-4 Sequence 4, Appl  
42 674.5 25.9 465 2 US-08-878-989-18 Sequence 18, Appl  
43 674.5 25.9 465 2 US-08-860-150-7 Sequence 7, Appl  
44 674.5 25.9 465 3 US-09-338-132-7 Sequence 7, Appl  
45 674.5 25.9 465 3 US-09-272-796-18 Sequence 18, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-804-471A-2  
; Sequence 2, Application US/09804471A  
; Patent No. 6479269  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-09-804-471A-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.4e-242;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLKFYKARNPLDAGAAEPIANRSLNLFQCKPFPMTQQOMSPSLREGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSFVRKYSDTIAELOPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELOPSAKDFEVRSLVGCCHFAEVQVREKATG 120

QY 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOVAFQDKNHLVLMVEYQPG 180  
DB 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOVAFQDKNHLVLMVEYQPG 180

QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVRDIPKPNILVDRTHGHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVRDIPKPNILVDRTHGHIKLVDF 240

QY 241 GSAAMKSNKMYNAKPIGTPDYMAPEVLTVNMGCKGYGLDCDWSGVYAYEMVYGR 300  
DB 241 GSAAMKSNKMYNAKPIGTPDYMAPEVLTVNMGCKGYGLDCDWSGVYAYEMVYGR 300

QY 301 SFFAEGTSARTNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKRLKEFGLCCHPFF 360  
DB 301 SFFAEGTSARTNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKRLKEFGLCCHPFF 360

QY 361 SKIDWNIRNSPPFPVTLKSDDDTSNDFPEPKSNWSSPCQLSPSFGSEELFPVFGFS 420

Db 361 SKIDWNIRNSPPFVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPFGVS 420  
Qy 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480  
Qy 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

RESULT 2  
US-10-238-709-2  
; Sequence 2, Application US/10238709  
; Patent No. 6680188  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-238-709-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.4e-242;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
Db 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
Qy 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Qy 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
Db 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDKGTGYGLDCDWSVGVIAEMYYGR 300  
Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDKGTGYGLDCDWSVGVIAEMYYGR 300  
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Db 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSSDFDLIOQLCGQKERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPFGVS 420  
Db 361 SKIDWNIRNSPPFVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPFGVS 420  
Qy 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480  
Qy 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

RESULT 3

US-10-028-946-4  
; Sequence 4, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1958  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-028-946-4

Query Match 93.8%; Score 2440; DB 4; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5e-226;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
Db 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
Qy 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Qy 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
Db 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDKGTGYGLDCDWSVGVIAEMYYGR 300  
Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDKGTGYGLDCDWSVGVIAEMYYGR 300  
Qy 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSSDFDLIOQLCGQKERLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSSDFDLIOQLCGQKERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPFGVS 420  
Db 361 SKIDWNIRNSPPFVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPFGVS 420  
Qy 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKV 468  
Db 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQSDQKCHKV 468

RESULT 4  
US-10-028-946-2  
; Sequence 2, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

Query Match      93.8%; Score 2440; DB 4; Length 2054;
Best Local Similarity 99.6%; Pred. No. 5.4e-226;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
QY 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
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DB 301 SPFAEGTSARTFNINMFORFLKPDPPKVSDDFLDIQSLICGOKERLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468
DB 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468

RESULT 5
US-09-804-471A-4
; Sequence 4, Application US/03804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-804-471A-4

Query Match      87.3%; Score 2271.5; DB 4; Length 494;
Best Local Similarity 87.3%; Pred. No. 1.2e-210;
Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

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DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
QY 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
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DB 301 SPFAEGTSARTFNINMFORFLKPDPPKVSDDFLDIQSLICGOKERLKFEGLCCHPFF 360
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DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468
DB 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468

RESULT 6
US-10-238-709-4
; Sequence 4, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-238-709-4

Query Match      87.3%; Score 2271.5; DB 4; Length 494;
Best Local Similarity 87.3%; Pred. No. 1.2e-210;
Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
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QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180
QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPENILVDRTHGHIKLVDF 240
QY 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
DB 241 GSAAKNSNKMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDWMSVGVIAEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKPDPPKVSDDFLDIQSLICGOKERLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKPDPPKVSDDFLDIQSLICGOKERLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468
DB 421 YSKALGILGRESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFI 468
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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2

Query Match 49.3%; Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Qy 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240
Qy 241 GSAAKMNSNMV 252
Db 241 GSAAKMNSNMV 252

RESULT 9
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-916-204-4

Query Match 45.3%; Score 1180; DB 4; Length 251;
Best Local Similarity 90.4%; Pred. No. 1.2e-105;
Matches 227; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGVNPNSEASAEPIASRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Qy 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Qy 241 GSAAKMNSNMV 252
Db 241 GSAAKMNSNMV 252

RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2

Query Match 49.3%; Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Qy 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Qy 241 GSAAKMNSNMV 252
Db 241 GSAAKMNSNMV 252

RESULT 9
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-09-916-204-4

Query Match 49.3%; Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSRREGILDALFVLFE 60
Qy 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Qy 241 GSAAKMNSNMV 252
Db 241 GSAAKMNSNMV 252

RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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; Sequence 5, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-5

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Best Local Similarity 90.0%; Pred. No. 2.3e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MLKFKYGRNPPEASASEPIASRSLNLFQKPPMTQQQMSALSREGMLDALFALFE 60
QY 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120
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QY 121 DIVAMKMKKALLAQEQVFFEBERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DIVAMKMKKALLAQEQVFFEBERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELIHAVSHVLMGVVHRDIPENILVDRTGHIKLVDF 240
DB 181 DFLSLNRYEDQDENLIQFYLAELIHAVSHVLMGVVHRDIPENILVDRTGHIKLVDF 240
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; Sequence 6, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-6

Query Match      45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.3e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MLKFKYGRNPPEASASEPIASRSLNLFQKPPMTQQQMSALSREGMLDALFALFE 60
QY 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120
DB 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120
QY 121 DIVAMKMKKALLAQEQVFFEBERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DIVAMKMKKALLAQEQVFFEBERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELIHAVSHVLMGVVHRDIPENILVDRTGHIKLVDF 240
DB 181 DFLSLNRYEDQDENLIQFYLAELIHAVSHVLMGVVHRDIPENILVDRTGHIKLVDF 240
QY 241 GSAAKKMSNKM 251
DB 241 GSAAKKMSNKM 251

RESULT 15
US-08-685-576-4
; Sequence 4, Application US/08685576
; Patent No. 5906819
; GENERAL INFORMATION:
; APPLICANT: Kaibuchi, Kozi
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Nakano, Takeshi
; APPLICANT: Ito, Masaaki
; APPLICANT: Takahashi, No. 5906819uaki
; TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/685,576
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-325129
; FILING DATE: 20-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-17150
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-131206
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16897/843
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-685-576-4

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Best Local Similarity 40.1%; Pred. No. 4.2e-74;
Matches 181; Conservative 97; Mismatches 141; Indels 32; Gaps 10;

QY 24 ASRLNLFQKPPFMTQQQMSPLSRREGILDALFVLECSOPALMKIKHVSFVRYKSDT 83

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Db 79 VKKIGLQMAEDYDVVKVIGRGAFGEVQLVRHKASQKVYAMKLLSKFEMIKRSDSAFPE 138  
Qy 144 EERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPGDLSLNLRYEDQIDENLIQFYLA 203  
Db 139 EERDIFAFANSPWVQLFYAFQDDRYLYMWYMPGGDLVNLMSNYD--VPERKAKFYTA 196  
Qy 204 ELILAVSHVLMGVVHRDIKPENLIVDRTHIKLIVDFGSAKONSKONNAKLPIGTDPY 263  
Db 197 EVLALDAIHSMLIHRDVKPDNMLLDKHGHLKLADFGTCMKMDDETGMVHCDTAVGTPDY 256  
Qy 264 MAPEVLTVMGDGGKGTGLOCDWMSVGVIAEMYIGRSPFAEGTSARTFNINKNFORFLK 323  
Db 257 ISPEVLKSQGGD--GFVGRCDWMSVGVFLYEMLVGDTFPYADSLVGYTSKINDHKNSLC 314  
Qy 324 PPDDPKVSDFLDLIOQLLQCGKRLKPEG---LCCHPFF--SKIDMNNIRNSPPFPVPT 378  
Db 315 FPEDAETSKHAKNLICAFLTDRVRLGRNGVEEIRQHPFFKNDQWHDNIRETAAPVPE 374  
Qy 379 LKSDDDTSNDEPEKNSM-VSSSPCQLSPSGRSGEELPFVGFYSXALGILGRSESVWSG 437  
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Qy 438 LDSFA--KTSMEKKLLIKSKELQDSQDKCH 466  
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Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 12:31:42 ; Search time 141 Seconds  
(without alignments)  
1245.059 Million cell updates/sec

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Perfect score: 2602  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications AA:\*
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  - 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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  - 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/prodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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  - 18: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2602	100.0	497	9	US-09-804-471A-2
2	2602	100.0	497	14	US-10-238-709-2
3	2602	100.0	497	15	US-10-724-594-2
4	2589	99.5	497	15	US-10-311-034-7
5	2440	93.8	623	15	US-10-262-511-4
6	2440	93.8	1958	13	US-10-028-946-4
7	2440	93.8	1958	17	US-10-791-666-4
8	2440	93.8	2054	13	US-10-028-946-2
9	2440	93.8	2054	15	US-10-415-011-21
10	2440	93.8	2054	17	US-10-791-666-2
11	2430	93.4	2053	13	US-10-017-216-2
12	2430	93.4	2053	14	US-10-325-430-12
13	2430	93.4	2053	17	US-10-757-262-52

14	2418.5	92.9	2055	17	US-10-618-941-67	Sequence 67, Appl
15	2412.5	92.7	2053	11	US-09-964-956-11	Sequence 11, Appl
16	2412.5	92.7	2053	15	US-10-262-511-2	Sequence 2, Appl
17	2412.5	92.7	2066	11	US-09-964-956-9	Sequence 9, Appl
18	2412.5	92.7	2066	15	US-10-262-511-14	Sequence 14, Appl
19	2271.5	87.3	494	9	US-09-804-471A-4	Sequence 4, Appl
20	2271.5	87.3	494	14	US-10-238-709-4	Sequence 4, Appl
21	2271.5	87.3	494	15	US-10-724-594-4	Sequence 4, Appl
22	2172.5	83.5	319	13	US-10-017-216-4	Sequence 4, Appl
23	1652	63.5	319	14	US-10-412-897-2	Sequence 2, Appl
24	1284	49.3	257	14	US-10-282-048-2	Sequence 2, Appl
25	1180	45.3	251	14	US-10-282-048-4	Sequence 4, Appl
26	1177	45.2	251	14	US-10-282-048-5	Sequence 5, Appl
27	932.5	35.8	1565	16	US-10-702-496-2	Sequence 6, Appl
28	929	35.7	475	15	US-10-415-011-2	Sequence 2, Appl
29	929	35.7	1572	14	US-10-333-314-20	Sequence 20, Appl
30	929	35.7	1572	17	US-10-618-941-68	Sequence 68, Appl
31	929	34.9	1548	14	US-10-369-493-6347	Sequence 6347, Ap
32	908.5	34.5	1000	14	US-10-012-697-1540	Sequence 1540, Ap
33	896.5	34.5	1711	9	US-09-771-161A-219	Sequence 219, App
34	896.5	34.5	1711	9	US-09-771-161A-220	Sequence 220, App
35	896.5	34.5	1711	15	US-10-399-225-10	Sequence 10, Appl
36	896.5	34.5	496	9	US-09-771-161A-228	Sequence 228, App
37	891	34.2	1719	14	US-10-288-798-2	Sequence 2, Appl
38	891	34.2	1719	15	US-10-362-892-2	Sequence 2, Appl
39	891	34.2	1770	15	US-10-433-794-19	Sequence 19, Appl
40	891	34.2	1572	16	US-10-702-496-4	Sequence 4, Appl
41	890	33.9	1664	15	US-10-210-130-102	Sequence 102, App
42	882.5	33.9	1738	15	US-10-210-130-100	Sequence 100, App
43	882.5	33.9	573	9	US-09-764-868-671	Sequence 671, App
44	877.5	33.7	573	11	US-09-764-875-1205	Sequence 1205, Ap
45	877.5	33.7	573	11	US-09-764-875-1205	Sequence 1205, Ap

ALIGNMENTS

RESULT 1

US-09-804-471A-2  
; Sequence 2, Application US/09804471A  
; Patent No. US20020132322A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-804-471A-2

Query Match	100.0%	Score 2602;	DB 9;	Length 497;
Best Local Similarity	100.0%	Pred. No. 1.9e-184;		
Matches 497;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLKFKYARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSREGILDALFVLFE	60	
Db	1	MLKFKYARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSREGILDALFVLFE	60	
Qy	61	ECSQALMKIKHVSNFVKYSDTTAEQLQPSAKDFEVRSLVGGHFAEVQVVRKATG	120	
Db	61	ECSQALMKIKHVSNFVKYSDTTAEQLQPSAKDFEVRSLVGGHFAEVQVVRKATG	120	
Qy	121	DIYAMKVNKKKALLAQEQVVSFEERNILSRSTSPWIPQIQYAFQDKNHLVLYMEYOPGG	180	
Db	121	DIYAMKVNKKKALLAQEQVVSFEERNILSRSTSPWIPQIQYAFQDKNHLVLYMEYOPGG	180	

181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240  
181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240  
241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300  
241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300  
301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360  
301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360  
361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420  
361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420  
421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
481 ILPSVYAKSGARGCWL 497  
481 ILPSVYAKSGARGCWL 497

RESULT 2  
US-10-238-709-2  
; Sequence 2, Application US/10238709  
; Publication No. US20030022340A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-238-709-2

Query Match 100.0%; Score 2602; DB 14; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.9e-184;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFYGARNPDLGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSREGILDALFVLE 60  
DB 1 MLKFYGARNPDLGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSREGILDALFVLE 60

QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120

QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180

QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300  
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300

QY 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420

QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480

QY 481 ILPSVYAKSGARGCWL 497  
DB 481 ILPSVYAKSGARGCWL 497

RESULT 3  
US-10-724-594-2  
; Sequence 2, Application US/10724594  
; Publication No. US20040091993A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV II  
; CURRENT APPLICATION NUMBER: US/10/724,594  
; CURRENT FILING DATE: 2003-12-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-724-594-2

Query Match 100.0%; Score 2602; DB 15; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.9e-184;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFYGARNPDLGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSREGILDALFVLE 60  
DB 1 MLKFYGARNPDLGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSREGILDALFVLE 60

QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120

QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180

QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSLMGVYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300  
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMVYGR 300

QY 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLQSLLCGQKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSSPCOLSPSGSGEELPFVGF 420

QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480

QY 481 ILPSVYAKSGARGCWL 497  
DB 481 ILPSVYAKSGARGCWL 497

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RESULT 4
US-10-311-034-7
; Sequence 7, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAPALIA, Apnil
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: KHO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: EI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,457; 60/215,651; 60/216,605; 60/218,372; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1
US-10-311-034-7

Query Match          99.5%; Score 2589; DB 15; Length 497;
Best Local Similarity 99.6%; Pred. No. 1.8e-183;
Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPTIANRSLNLFQCKPPFMTQQQMSPLRSRGILDALFVLPE 60
Db 1 MLKFKYGARNPLDAGAAEPTIASRSLNLFQCKPPFMTQQQMSPLRSRGILDALFVLPE 60
Qy 61 ECSQPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGCQHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGCQHFAEVQVREKATG 120

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RESULT 5
US-10-262-511-4
; Sequence 4, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Willet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Sheroy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09

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Qy 121 DIYAKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYARQDKNHLYLVMEYOPGG 180
Db 121 DIYAKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYARQDKNHLYLVMEYOPGG 180
Qy 181 DLLSILNRYEDQDENLTIQFYLAELIILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240
Db 181 DLLSILNRYEDQDENLTIQFYLAELIILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240
Qy 241 GSAAKMSNKVNAKLPIGTPDYNAPEVLTVNMGDGKTYGLDCDMSVGVIAEMTYGR 300
Db 241 GSAAKMSNKVNAKLPIGTPDYNAPEVLTVNMGDGKTYGLDCDMSVGVIAEMTYGR 300
Qy 301 SPFAEGTSARTFNIMNFQRELKFPDPPKVSDDFLDLTIQSLCCQKERLKEGELCCHPFF 360
Db 301 SPFAEGTSARTFNIMNFQRELKFPDPPKVSDDFLDLTIQSLCCQKERLKEGELCCHPFF 360
Qy 361 SKIDWNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
Db 361 SKIDWNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQDKCHKVFIISAAGLLPCSR 480
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQDKCHKVFIISAAGLLPCSR 480
Qy 481 ILPSVYAKGSARGRCWL 497
Db 481 ILPSVYAKGSARGRCWL 497

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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-511-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 15; Length 623;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASLNLFPOGKPPFMTQQQMSPLSRGILDALFVLPE 60
DB 5 MLKFKYGARNPLDAGAAEPIASRASLNLFPOGKPPFMTQQQMSPLSRGILDALFVLPE 64
QY 61 ECSQPALMKIKHVSNFVRKYSYDTIABQLQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
DB 65 ECSQPALMKIKHVSNFVRKYSYDTIABQLQPSAKDFEVRSLVGCCHFAEVQVREKATG 124
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
DB 125 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 184
QY 181 DLSLLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
DB 185 DLSLLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 244
QY 241 GSAAKMNSKNVNAKPIGTPDYMAPEVLTVMGDKGTGYGLDCDWMSVGVIAEMMYGR 300
DB 245 GSAAKMNSKNVNAKPIGTPDYMAPEVLTVMGDKGTGYGLDCDWMSVGVIAEMMYGR 304
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLQSLCCGOKERLKEGLCCHPFF 360
DB 305 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLQSLCCGOKERLKEGLCCHPFF 364
QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEPEKNWSVSSPCQLSPSGFSGEELPFVGF 420
DB 365 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEPEKNWSVSSPCQLSPSGFSGEELPFVGF 424
QY 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKV 468
DB 425 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKM 472

RESULT 6
US-10-028-946-4
; Sequence 4, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-028-946-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 17; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-028-946-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 13; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASLNLFPOGKPPFMTQQQMSPLSRGILDALFVLPE 60
DB 1 MLKFKYGARNPLDAGAAEPIASRASLNLFPOGKPPFMTQQQMSPLSRGILDALFVLPE 60
QY 61 ECSQPALMKIKHVSNFVRKYSYDTIABQLQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSYDTIABQLQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
QY 181 DLSLLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
DB 181 DLSLLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
QY 241 GSAAKMNSKNVNAKPIGTPDYMAPEVLTVMGDKGTGYGLDCDWMSVGVIAEMMYGR 300
DB 241 GSAAKMNSKNVNAKPIGTPDYMAPEVLTVMGDKGTGYGLDCDWMSVGVIAEMMYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLQSLCCGOKERLKEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLQSLCCGOKERLKEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEPEKNWSVSSPCQLSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEPEKNWSVSSPCQLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKV 468
DB 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKM 468

RESULT 7
US-10-791-666-4
; Sequence 4, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-791-666-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 17; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLE 60
Db 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKWKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVYQPGG 180
Db 121 DIYAMKWKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVYQPGG 180
QY 181 DLLSLNRYEQDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
Db 181 DLLSLNRYEQDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMWSVGVIAEYMIYGR 300
Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMWSVGVIAEYMIYGR 300
QY 301 SPFAEGTSARTFNINMFQFLKFPDDPKYSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMFQFLKFPDDPKYSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPCQSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPCQSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468

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RESULT 8

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US-10-028-946-2
; Sequence 2, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

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Query Match 93.8%; Score 2440; DB 13; Length 2054;
Best Local Similarity 99.6%; Pred. No. 1.1e-171;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLE 60
Db 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKWKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVYQPGG 180
Db 121 DIYAMKWKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVYQPGG 180
QY 181 DLLSLNRYEQDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240

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Db 181 DLLSLNRYEQDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMWSVGVIAEYMIYGR 300
Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMWSVGVIAEYMIYGR 300
QY 301 SPFAEGTSARTFNINMFQFLKFPDDPKYSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMFQFLKFPDDPKYSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPCQSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPCQSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468

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RESULT 9

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US-10-415-011-21
; Sequence 21, Application US/10415011
; Publication No. US2004005394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01

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; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Insite ID No. US20040053394A1 7484498CD1
US-10-415-011-21

Query Match          93.8%; Score 2440; DB 15; Length 2054;
Best Local Similarity 99.6%; Pred. No. 1.1e-171;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180

QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLNGYVHRDIKPNILVDRTHIKLVDF 240
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLNGYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSGVIAIYEMIGR 300
DB 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSGVIAIYEMIGR 300

QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIOQLLGGQKERLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIOQLLGGQKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNWSVSSPCQLSPGSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNWSVSSPCQLSPGSGEELPFVGF 420

QY 421 YSKALGILGRSESVSGLDSPAKTSMEXKLLIKSKELQDSQDKCHKV 468
DB 421 YSKALGILGRSESVSGLDSPAKTSMEXKLLIKSKELQDSQDKCHKV 468

RESULT 10
US-10-791-666-2
; Sequence 2, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Kuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-791-666-2

Query Match          93.8%; Score 2440; DB 17; Length 2054;

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Best Local Similarity 99.6%; Pred. No. 1.1e-171;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180

QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLNGYVHRDIKPNILVDRTHIKLVDF 240
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLNGYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSGVIAIYEMIGR 300
DB 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSGVIAIYEMIGR 300

QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIOQLLGGQKERLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIOQLLGGQKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNWSVSSPCQLSPGSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNWSVSSPCQLSPGSGEELPFVGF 420

QY 421 YSKALGILGRSESVSGLDSPAKTSMEXKLLIKSKELQDSQDKCHKV 468
DB 421 YSKALGILGRSESVSGLDSPAKTSMEXKLLIKSKELQDSQDKCHKV 468

RESULT 11
US-10-017-216-2
; Sequence 2, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prote
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-216-2

Query Match          93.4%; Score 2430; DB 13; Length 2053;
Best Local Similarity 99.1%; Pred. No. 6.1e-171;
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180

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QY 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVHLMGVYHRDIKPENILVDRTHIKLVDP 240  
DB 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVHLMGVYHRDIKPENILVDRTHIKLVDP 240  
QY 241 GSAAKMNSNKNVNAKLPIGTPDYMABEVLTVNMGDKGTGYGLDCDMSVGVIAIYEMMYGR 300  
DB 241 GSAAKMNSNKNVNAKLPIGTPDYMABEVLTVNMGDKGTGYGLDCDMSVGVIAIYEMMYGR 300  
QY 301 SPFAEGTSARTENNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTENNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420  
DB 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
RESULT 12  
US-10-325-430-12  
; Sequence 12, Application US/10325430  
; Publication No. US20030135325A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; FILE REFERENCE: 32838,336 and 52908  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-325-430-12  
Query Match 93.4%; Score 2430; DB 14; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.1e-171;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQOQMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQOQMSPLSREGILDALFVLFE 60  
QY 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGCHFAEVQVVRKATG 120  
DB 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGCHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
DB 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
QY 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVHLMGVYHRDIKPENILVDRTHIKLVDP 240  
DB 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVHLMGVYHRDIKPENILVDRTHIKLVDP 240  
QY 241 GSAAKMNSNKNVNAKLPIGTPDYMABEVLTVNMGDKGTGYGLDCDMSVGVIAIYEMMYGR 300  
DB 241 GSAAKMNSNKNVNAKLPIGTPDYMABEVLTVNMGDKGTGYGLDCDMSVGVIAIYEMMYGR 300  
QY 301 SPFAEGTSARTENNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTENNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQERLKFEGLCCHPFF 360

QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420  
DB 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
RESULT 13  
US-10-757-262-52  
; Sequence 52, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE REFERENCE: MPI03-007P1RNMNM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332  
; PRIOR FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-757-262-52  
Query Match 93.4%; Score 2430; DB 17; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.1e-171;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQOQMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQOQMSPLSREGILDALFVLFE 60  
QY 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGCHFAEVQVVRKATG 120  
DB 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGCHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
DB 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180



Qy	1	MLKFKYCARNPLDAGAAETIANEASRLNLFQCKPPEMTQOQMSPLSREGIILDALFVLEE	60
Db	1	MLKFKYCARNPLDAGAAETIANEASRLNLFQCKPPEMTQOQMSPLSREGIILDALFVLEE	60
Qy	61	ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG	120
Db	61	ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG	120
Qy	121	DIYAMKMKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG	180
Db	121	DIYAMKMKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG	180
Qy	181	DLISLLNRYEDQDENLIQFYLAELILAVHSVHMGYVHRDIKPENILVDRTHIKLVDF	240
Db	181	DLISLLNRYEDQDENLIQFYLAELILAVHSVHMGYVHRDIKPENILVDRTHIKLVDF	240
Qy	241	GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEMIYGR	300
Db	241	GSAAKMNSNK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEMIYGR	299
Qy	301	SPEAGTSARTFNINNFQFLKFPDDPKVSSDFDLIOSLLCGQKERLKFEGLCCHPFF	360
Db	300	SPEAGTSARTFNINNFQFLKFPDDPKVSSDFDLIOSLLCGQKERLKFEGLCCHPFF	359
Qy	361	SKIDWNIRNSPPFPVPTLKSDDTNSNFDPEKNSWVSSPCQLSPSPGSGBELPFVGFS	420
Db	360	SKIDWNIRNAPPPFPVPTLKSDDTNSNFDPEKNSWVSSPCQLSPSPGSGBELPFVGFS	419
Qy	421	YSKALGILGRSESVVSGLDSPAKTSSMEKKLILIKSKELQDSQDKCHKV	468
Db	420	YSKALGILGRSESVVSGLDSPAKTSSMEKKLILIKSKELQDSQDKCHKM	467

Search completed: November 8, 2004, 12:43:48  
Job time : 144 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 07:38:21 ; Search time 774 Seconds  
(without alignments)  
10538.677 Million cell updates/sec

Title: US-10-724-594-1

Perfect score: 1515

Sequence: 1 999gaagattgaagttcaa.....tctgagccgctgataccgta 1515

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
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17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	1515	100.0	1515	US-10-238-709-1	Sequence 1, Appli
3	1515	100.0	1515	US-10-724-594-1	Sequence 1, Appli
4	1510.2	99.7	2056	US-10-311-034-33	Sequence 33, Appli
5	1404.2	92.7	6298	US-10-415-011-43	Sequence 43, Appli
6	1398.2	92.3	1870	US-10-262-511-3	Sequence 3, Appli
7	1398.2	92.3	5877	US-10-028-946-3	Sequence 3, Appli
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15 1391.8 91.9 6162 15 US-10-325-430-11 Sequence 11, Appli  
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18 1375.8 90.8 6189 16 US-10-262-511-1 Sequence 1, Appli  
19 1375.8 90.8 6201 11 US-09-964-356-8 Sequence 8, Appli  
20 1375.8 90.8 6201 16 US-10-262-511-13 Sequence 13, Appli  
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27 246.8 16.3 5438 18 US-10-618-941-2 Sequence 2, Appli  
28 240 15.8 6335 16 US-10-388-934-85 Sequence 85, Appli  
29 238.8 15.8 5373 17 US-10-702-496-5 Sequence 5, Appli  
30 236.8 15.6 4917 17 US-10-385-163-121 Sequence 121, Appli  
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42 216.2 14.3 174493 9 US-09-804-471A-3 Sequence 3, Appli  
43 216.2 14.3 174493 14 US-10-238-709-3 Sequence 3, Appli  
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45 214.4 14.2 1479 9 US-09-771-161A-46 Sequence 46, Appli

## ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/09804471A  
; Patent No. US20020132322A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-471A-1

Query Match 100.0%; Score 1515; DB 9; Length 1515;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 CCCATTGCCAACCGGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATG 120  
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1141 CTCAGTCCGAGATGACACCTCCAAATTTTGAATGACACAGAGAAATTCGTGGTTCA 1200
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1381 CAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGACGCGGCTCTCTCTTC 1440
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1441 TCAGAGATCTCTCCGCTGATATGCAAGAGGATCCGCGGCGGCTGCTGGCTCTGA 1500
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; Sequence 1, Application US/10238709
; Publication No. US20030022340A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-10-238-709-1

Query Match 100.0%; Score 1515; DB 14; Length 1515;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 60
DB 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 60
QY 61 CCCATTGCCAACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTATG 120
DB 61 CCCATTGCCAACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTATG 120
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US-10-724-594-1  
 ; Sequence 1, Application US/10724594  
 ; Publication No. US20040091993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE REFERENCE: CL001164DIV II  
 ; CURRENT APPLICATION NUMBER: US/10724,594  
 ; CURRENT FILING DATE: 2003-12-02  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1515  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-724-594-1

Query Match 100.0%; Score 1515; DB 16; Length 1515;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 CATCGAGACATCAAGCTGAGAACATTCGTGTGACCGCACAGGACACATCAAGCTGGT 720
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Db 781 GGGACCCAGATTTACATGCTCTCTGAGTGTCTGACTGTGATGAACGGGGATGGAAGGC 840
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Db 1081 TTCTTCTTAAATTTGACTGTGAACAACTTCCTTAATTCCTCTCTCTCTCTCTCTCTCT 1140
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Db 1141 CTCAGTCCGAGTGAACCTCCATTTTGTATGAACAGAGAAATTCGTGGGTTTCA 1200
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RESULT 4

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US-10-311-034-33
; Sequence 33, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.

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; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIFON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-08-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33

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Query Match 99.7%; Score 1510.2; DB 16; Length 2066;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 8 GGGGAGATGTTGAAGTTCAAATATGAGGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 67
Qy 61 CCATTGCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120
Db 68 CCATTGCCAGCGCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 127
Qy 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGATATAGATCCCTCTTTGTTCTC 180
Db 128 ACTCAACAGCAGATGCTCTCTTTCCGAGAGGATATAGATCCCTCTTTGTTCTC 187
Qy 181 TTTTGAAGAATGACGCTGCTCTGATCAAGATTAACAGCTGAGCAACTTTGTCGG 240
Db 188 TTTTGAAGAATGACGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 247
Qy 241 AAGTATCCGACACCATAGCTGAGTTACAGGAGCTCCAGGCTCCGCAAGGACTTCGAA 300
Db 248 AAGTATCCGACACCATAGCTGAGTTACAGGAGCTCCAGGCTCCGCAAGGACTTCGAA 307
Qy 301 GTCAGAAAGTCTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGGTAAAGAGAAAGA 360

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Db	308	GT	CAGAAGTCTTGTAGTGTGGTCACTTTGCTCGAATGCGAGTGGGTAAAGAGAGAAAGCA	367
Qy	361	ACC	GGGACATCTATGCTATGAAGTATGAAGAAGAGGCTTTATTTGGCCCGAGGACAG	420
Db	368	ACC	GGGACATCTATGCTATGAAGTATGAAGAAGAGGCTTTATTTGGCCCGAGGACAG	427
Qy	421	GT	TTTCATTTTGGAGAGCGGAAATATTATCTCGAAGCACAAAGCCGCTGGATCCCC	480
Db	428	GT	TTTCAATTTTGGAGAGCGGAAATATTATCTCGAAGCACAAAGCCGCTGGATCCCC	487
Qy	481	CA	ATTACAGTATGCTTTTCAGGACAAAAATCACCTTTATCTGGTCACTGGAATATCACGCT	540
Db	488	CA	ATTACAGTATGCTTTTCAGGACAAAAATCACCTTTATCTGGTCACTGGAATATCACGCT	547
Qy	541	GG	AGGACCTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAACACCTGATA	600
Db	548	GG	AGGACCTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAACACCTGATA	607
Qy	601	CAG	TTTTACCTAGCTGAGCTGATTTTGGCTGTTCCACAGCGTTCACTGATGGGATAGCTG	660
Db	608	CAG	TTTTACCTAGCTGAGCTGATTTTGGCTGTTCCACAGCGTTCACTGATGGGATAGCTG	667
Qy	661	CAT	CGACATCAAGCTCTGAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTG	720
Db	668	CAT	CGACATCAAGCTCTGAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTG	727
Qy	721	GAT	TTTGGATCTGCCGCGAAATCAATTTCAAAACAAGATGGTGAATGCCAACTCCCGATT	780
Db	728	GAT	TTTGGATCTGCCGCGAAATCAATTTCAAAACAAGATGGTGAATGCCAACTCCCGATT	787
Qy	781	GG	ACCCAGATTAACATGGCTCCTGAAGTGTGCTGTGATGAACGGGGATGAAAAGGC	840
Db	788	GG	ACCCAGATTAACATGGCTCCTGAAGTGTGCTGTGATGAACGGGGATGAAAAGGC	847
Qy	841	AC	TACGGCTGGACTGCTGCTGCTCAGTGGCGTGATTCGCTATGATGATGATTTAT	900
Db	848	AC	TACGGCTGGACTGCTGCTGCTCAGTGGCGTGATTCGCTATGATGATGATTTAT	907
Qy	901	GG	GAGATCCCCCTTTTCGACAGGGAACCTCTGCCAGAACCTTTCAATAACATTAATGAATTC	960
Db	908	GG	GAGATCCCCCTTTTCGACAGGGAACCTCTGCCAGAACCTTTCAATAACATTAATGAATTC	967
Qy	961	CAG	GGTTTTTGAATTTCCAGATGAACCCAAAGTGACAGTGACTTTCTTGATCTGATTT	1020
Db	968	CAG	GGTTTTTGAATTTCCAGATGAACCCAAAGTGACAGTGACTTTCTTGATCTGATTT	1027
Qy	1021	CA	AAGCTTGTGTGCGGCCAGAAAGACAGACTGAAGTTTCAAGTGCTTTTGCCTCCATCCT	1080
Db	1028	CA	AAGCTTGTGTGCGGCCAGAAAGACAGACTGAAGTTTCAAGTGCTTTTGCCTCCATCCT	1087
Qy	1081	TT	CTTCTCTAAAATTGACTGGAAACAATTCGTAACCTCTCCTCCCCCTTCGTTCCCAACC	1140
Db	1088	TT	CTTCTCTAAAATTGACTGGAAACAATTCGTAACCTCTCCTCCCCCTTCGTTCCCAACC	1147
Qy	1141	CT	CAAGTCCGACGATGACCTCCAAATTTTGAATGAACACAGAGAGATTCGTCGGTTTCA	1200
Db	1148	CT	CAAGTCTGACGATGACCTCCAAATTTTGAATGAACACAGAGAGAAATTCGTGGGTTTCA	1207
Qy	1201	TC	CTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGG	1260
Db	1208	TC	CTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGG	1267
Qy	1261	TTTT	TCGTACAGCAAGGACCTGGGATTTCTTGGTATGATCTGATCTGTTGTGCGGTCGTG	1320
Db	1268	TTTT	TCGTACAGCAAGGACCTGGGATTTCTTGGTATGATCTGATCTGTTGTGCGGTCGTG	1327
Qy	1321	GAC	TCCCTCTCAGAGCTAGCTCCATCGAAAAAGAACTTCTCATCAAAAGCAAGAGCTA	1380
Db	1328	GAC	TCCCTCTCAGAGCTAGCTCCATCGAAAAAGAACTTCTCATCAAAAGCAAGAGCTA	1387
Qy	1381	CAG	ACTCTCAGGACAGTGTCAAGAGTATTTATTTTCGAGCGCGGCTCTCTTCTCTGTC	1440
Db	1388	CAG	ACTCTCAGGACAGTGTCAAGAGTATTTATTTTCGAGCGCGGCTCTCTTCTCTGTC	1447

Qy	1441	TCCAGGATCTCCCGTCCGTATATGCCAAGGGATCGCCCGGGGCGCTGCTGGCTCTGA	1500
Db	1448	TCCAGGATCTCCCGTCCGTATATGCCAAGGGATCGCCCGGGGCGCTGCTGGCTCTGA	1507
Qy	1501	GCGCCCTGATCCGTA	1515
Db	1508	GCGCCCTGATCCGTA	1522

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RESULT 5
US-10-415-011-43
; Sequence 43, Application US/10415011
; Publication No. US200400539441
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAVKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOWORSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 43
; LENGTH: 6298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US2004040
US-10-415-011-43

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Query Match	92.7%	Score 1404.2	DB 16	Length 6298
Best Local Similarity	95.8%	Pred. No. 0		
Matches 1406	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY	1	GGG	GAG	ATG	TG	AG	TT	CA	AT	TG	AG	CG	CG	GA	AT	CT	TT	TG	GA	TG	CT	TG	GT	GT	CT	G	TA	60	
Db	49	GGG	GAG	ATG	TG	AG	TT	CA	AT	TG	AG	CG	CG	GA	AT	CT	TT	TG	GA	TG	CT	TG	GT	GT	CT	G	TA	108	
QY	61	CCC	ATT	CC	AA	CGG	GCT	CA	AG	CT	CA	AA	TCT	GT	TT	CT	T	CC	AG	G	GA	AA	CC	AC	CC	TT	T	AT	120
Db	109	CCC	ATT	CC	CA	CGG	GCT	CA	AG	CT	CA	AA	TCT	GT	TT	CT	T	CC	AG	G	GA	AA	CC	AC	CC	TT	T	AT	168
QY	121	ACT	CA	AG	CAG	AG	AT	GT	CT	CT	TT	CC	G	AG	AG	G	G	AT	T	AG	AT	G	AT	G	CC	CT	TT	T	180
Db	169	ACT	CA	AG	CAG	AG	AT	GT	CT	CT	TT	CC	G	AG	AG	G	AT	T	AG	AT	G	AT	G	CC	CT	TT	T	128	
QY	181	TTT	GA	AA	TG	CAG	TG	CT	CT	CT	GAT	GA	AG	AT	T	AA	G	C	AG	C	AG	CA	CT	TT	T	G	C	240	
Db	229	TTT	GA	AA	TG	CAG	TG	CT	CT	CT	GAT	GA	AG	AT	T	AA	G	C	AG	C	AG	CA	CT	TT	T	G	C	288	
QY	241	AG	T	AT	CC	GAC	CA	CT	AG	T	GA	AG	T	CA	G	AG	CT	CC	AG	C	CT	CG	CA	AA	AG	G	AT	CG	300
Db	289	AG	T	AT	CC	GAC	CA	CT	AG	T	GA	AG	T	CA	G	AG	CT	CC	AG	C	CT	CG	CA	AA	AG	G	AT	CG	348
QY	301	G	T	C	A	A	A	G	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	360
Db	349	G	T	C	A	A	A	G	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	408
QY	361	ACC	GG	G	A	C	A	T	C	T	A	T	G	A	A	G	A	A	G	G	C	T	T	A	T	T	G	G	420
Db	409	ACC	GG	G	A	C	A	T	C	T	A	T	G	A	A	G	A	A	G	G	C	T	T	A	T	T	G	G	468
QY	421	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	480	
Db	469	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	528	
QY	481	CA	A	T	T	C	A	G	T	A	T	G	C	T	T	T	C	A	G	A	A	A	T	C	T	T	A	T	540
Db	529	CA	A	T	T	C	A	G	T	A	T	G	C	T	T	T	C	A	G	A	A	A	T	C	T	T	A	T	588
QY	541	G	G	A	G	G	A	C	T	T	G	T	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	600
Db	589	G	G	A	G	G	A	C	T	T	G	T	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	648
QY	601	C	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	660	
Db	649	C	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	708	
QY	661	C	A	T	C	G	A	C	A	T	C	A	A	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	720
Db	709	C	A	T	C	G	A	C</																					

RESULT 6  
US-10-262-511-3  
Sequence 3, Application US/10262511  
Publication No. US20040038223A1  
GENERAL INFORMATION:  
APPLICANT: Smithson, Glenna  
APPLICANT: Millet, Isabelle  
APPLICANT: Payman, John A.  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Ju, Jingfang  
APPLICANT: Li, Li  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Patturajan, Meera  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Ellerman, Karen  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Ort, Tatiana  
APPLICANT: Gorman, Linda  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Catterton, Elina  
APPLICANT: Ji, Weizhen  
APPLICANT: Miller, Charles E.  
APPLICANT: Rastelli, Luca  
APPLICANT: Stone, David J.  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Rothenberg, Mark E.  
APPLICANT: Leach, Martin D.  
APPLICANT: Agee, Michele L.  
APPLICANT: Berghs, Constance  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEOTIDE SEQUENCES  
FILE REFERENCE: 21402-462C  
CURRENT APPLICATION NUMBER: US/10/262,511  
CURRENT FILING DATE: 2003-05-28  
PRIOR APPLICATION NUMBER: 60/326,483  
PRIOR FILING DATE: 2004-10-02  
PRIOR APPLICATION NUMBER: 60/373,815  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 60/327,917  
PRIOR FILING DATE: 2001-10-09

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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequid version 0.1
; SEQ ID NO 3
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3

Query Match          92.3%; Score 1398.2; DB 16; Length 1870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGTAACCCATT 66
DB 14 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGTAACCCATT 73

QY 67 GCCAACCGGCGCTCCAGGCTGAATCTGCTCCAGCGGAAACCCCTTATGACTCAA 126
DB 74 GCCAGCGGCGCTCCAGGCTGAATCTGCTCCAGCGGAAACCCCTTATGACTCAA 133

QY 127 CAGCAGATGCTCCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTTTGAA 186
DB 134 CAGCAGATGCTCCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTTTGAA 193

QY 187 GAATGAGTCAAGCTGCTGATGAAGATTAAGCAGTGAAGCACTTTGTCGGAAGTAT 246
DB 194 GAATGAGTCAAGCTGCTGATGAAGATTAAGCAGTGAAGCACTTTGTCGGAAGTAT 253

QY 247 TCCGACACCATAGCTGATGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTGGAAGTCAGA 306
DB 254 TCCGACACCATAGCTGATGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTGGAAGTCAGA 313

QY 307 AGTCTTGATGTTGCTGCTACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG 366
DB 314 AGTCTTGATGTTGCTGCTACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG 373

QY 367 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGCGCCAGGAGGATTTCA 426
DB 374 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGCGCCAGGAGGATTTCA 433

QY 427 TTTTGTGAGGAGAGCGGCAATATTATCTCGAAGCACAAGCCCGTGGATCCGCCAATTA 486
DB 434 TTTTGTGAGGAGAGCGGCAATATTATCTCGAAGCACAAGCCCGTGGATCCGCCAATTA 493

QY 487 CAGTATGCTTTCCAGGACAAATATACCTTTATCTGTCATGGAATATCAGCTGGAGG 546
DB 494 CAGTATGCTTTCCAGGACAAATATACCTTTATCTGTCATGGAATATCAGCTGGAGG 553

QY 547 GACTTGTGCTCATTTTGAATAGATATGAGGACAGTATGATGCAAAACCTTGATACAGTTT 606
DB 554 GACTTGTGCTCATTTTGAATAGATATGAGGACAGTATGATGCAAAACCTTGATACAGTTT 613

QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCTATGATGGGATACGTGATCGA 666
DB 614 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCTATGATGGGATACGTGATCGA 673

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RESULT 7

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US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA

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QY 667 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
DB 674 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 733

QY 727 GGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTTGGGACC 786
DB 734 GGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTTGGGACC 793

QY 787 CCAGATTACATGGCTCCTCTGAAAGTGTGACTGTGATGAACGGGGATGGAAGGACCTTAC 846
DB 794 CCAGATTACATGGCTCCTCTGAAAGTGTGACTGTGATGAACGGGGATGGAAGGACCTTAC 853

QY 847 GGCCTGGACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
DB 854 GGCCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913

QY 907 TCCCGCTTTCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 966
DB 914 TCCCGCTTTCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 973

QY 967 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1026
DB 974 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1033

QY 1027 TTGTTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCCTTTCTTC 1086
DB 1034 TTGTTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCCTTTCTTC 1093

QY 1087 TCTAAATTTGACTGGAACAACATTCGTAATCTCTCTCCCGCTTTCGTTCCCACTTCAAG 1146
DB 1094 TCTAAATTTGACTGGAACAACATTCGTAATCTCTCTCCCGCTTTCGTTCCCACTTCAAG 1153

QY 1147 TCCGAGATGACACTCCCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1206
DB 1154 TCCGAGATGACACTCCCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1213

QY 1207 CCGTCCAGCTGAGCGCTTCCAGGCTTCTCGGGTGAAGAACTGCGGCTTTTGGGGTTCG 1266
DB 1214 CCGTCCAGCTGAGCGCTTCCAGGCTTCTCGGGTGAAGAACTGCGGCTTTTGGGGTTCG 1273

QY 1267 TACAGCAGGACCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTTGCTGGTCTGACTCC 1326
DB 1274 TACAGCAGGACCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTTGCTGGTCTGACTCC 1333

QY 1327 CCGTCCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1386
DB 1334 CCGTCCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1393

QY 1387 TCTCAGGACAAAGTGTCAAGGT 1409
DB 1394 TCTCAGGACAAAGTGTCAAGAT 1416

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Db 181 GAATGAGTCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240  
Qy 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGACTTCGAAGTCAGA 306  
Db 241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGACTTCGAAGTCAGA 300  
Qy 307 AGCTTGTAGTGTGTGCTCACTTTGTCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG 366  
Db 301 AGCTTGTAGTGTGTGCTCACTTTGTCTGAAGTGCAGGTGTTAAGAGAGAAAGCAACCGGG 360  
Qy 367 GACATCTATGCTATGAAGTGAAGCAAGAAAGGCTTTATGGCCCGAGAGAGGTTTCA 426  
Db 361 GACATCTATGCTATGAAGTGAAGCAAGAAAGGCTTTATGGCCCGAGAGAGGTTTCA 420  
Qy 427 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA 486  
Db 421 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA 480  
Qy 487 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTCATGAATATCAGCTCGAGGG 546  
Db 481 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTCATGAATATCAGCTCGAGGG 540  
Qy 547 GACTTGTGTCACCTTTTGAATAGATGAGGACCACTTATCTGTGTCATGAATATCAGCTCG 606  
Db 541 GACTTGTGTCACCTTTTGAATAGATGAGGACCACTTATCTGTGTCATGAATATCAGCTCG 600  
Qy 607 TACTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCATCTGATGGGATACGTGCATCGA 666  
Db 601 TACTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTCATCTGATGGGATACGTGCATCGA 660  
Qy 667 GACATCAAGCTGAGACATCTCGTGAAGCGGACACAGGACATCAAGCTGTGGATTTT 726  
Db 661 GACATCAAGCTGAGACATCTCGTGAAGCGGACACAGGACATCAAGCTGTGGATTTT 720  
Qy 727 GGATCTCCCGGAAAATGAATCAAAAGATGATGAAATGCCAAATCCCGATTTGGAGC 786  
Db 721 GGATCTCCCGGAAAATGAATCAAAAGATGATGAAATGCCAAATCCCGATTTGGAGC 780  
Qy 787 CCAGATTACATGGCTCTGAAGTGTGACTGTGATGAACGGGATGAAAGGACCACTAC 846  
Db 781 CCAGATTACATGGCTCTGAAGTGTGACTGTGATGAACGGGATGAAAGGACCACTAC 840  
Qy 847 GGCTGACTGTGACTGTGCTGCTGAGTGGGCTGATTGCCCTATGAGATGATTTATGGAGA 906  
Db 841 GGCTGACTGTGACTGTGCTGAGTGGGCTGATTGCCCTATGAGATGATTTATGGAGA 900  
Qy 907 TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 966  
Db 901 TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 960  
Qy 967 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGTGATCTGATTTCAAGC 1026  
Db 961 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGTGATCTGATTTCAAGC 1020  
Qy 1027 TTGTGTGCGGCGAGAAAGAGACTGAAGTTTGAAGGCTTTTGTGCGCATCTTTCTTC 1086  
Db 1021 TTGTGTGCGGCGAGAAAGAGACTGAAGTTTGAAGGCTTTTGTGCGCATCTTTCTTC 1080  
Qy 1087 TCTAAAATTCAGTGAAGCAACATTCGTAATCTCTCCCGCTTCTGTTCCCGCTCTCAAG 1146  
Db 1081 TCTAAAATTCAGTGAAGCAACATTCGTAATCTCTCTCCCGCTTCTGTTCCCGCTCTCAAG 1140  
Qy 1147 TCCGACGATGACACCTTCCAAATTTTGAATGACACAGAGAGAAATTCGTGGGTTTCATCCTCT 1206  
Db 1141 TCTGACGATGACACCTTCCAAATTTTGAATGACACAGAGAGAAATTCGTGGGTTTCATCCTCT 1200  
Qy 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTGTGGGGTTTTCG 1266  
Db 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTGTGGGGTTTTCG 1260  
Qy 1267 TACAGCAAGGCACTGGGGATCTTGTGTAGATCTGAGTCTGTTGTGTCGGGCTCGACTCC 1326  
Db 1261 TACAGCAAGGCACTGGGGATCTTGTGTAGATCTGAGTCTGTTGTGTCGGGCTCGACTCC 1320

Qy 1327 CCTGCCAAGACTAGCTCCATCGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1386  
Db 1321 CTGCGCAAGACTAGCTCCATCGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1380  
Qy 1387 TCTCAGGACAAAGTGTCACAAGGT 1409  
Db 1381 TCTCAGGACAAAGTGTCACAAGAT 1403

## RESULT 9

US-10-028-946-1  
; Sequence 1, Application US/10028946  
; Publication No. US20020123622A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Fridgde, Carl Johan  
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6165  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-028-946-1

Query Match 92.3%; Score 1398.2; DB 13; Length 6165;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGCTGAACCCATT 66  
Db 1 ATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGCTGAACCCATT 60  
Qy 67 GCCAACCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCAA 126  
Db 61 GCCACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCAA 120  
Qy 127 CAGCAGATGCTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTCTTTGAA 186  
Db 121 CAGCAGATGCTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTGTTCTCTTTGAA 180  
Qy 187 GAATGCACTCAGCTGCTCTGATGAAGATTAAAGCACTGAGCACTTTGTCGGAAGTAT 246  
Db 181 GAATGCACTCAGCTGCTCTGATGAAGATTAAAGCACTGAGCACTTTGTCGGAAGTAT 240  
Qy 247 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTCAGA 306  
Db 241 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTCAGA 300  
Qy 307 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 366  
Db 301 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360  
Qy 367 GACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 426  
Db 361 GACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
Qy 427 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA 486  
Db 421 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA 480  
Qy 487 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTCATGAATATCAGCTCGAGGG 546  
Db 481 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTCATGAATATCAGCTCGAGGG 540  
Qy 547 GACTTGTGTCACCTTTTGAATAGATGAGGACCACTTATCTGTGTCATGAATATCAGCTCG 606

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Db 541 GACCTGCTGCTCACTTTTGAATAGATATAGGACCACTAGATGAAACCTGATACAGTTT 600
QY 607 TACCTAGCTGAGCTGATTTGGCTGTTACACGGTTTCATCTGATGGATAGTGCATCGA 666
Db 601 TACCTAGCTGAGCTGATTTGGCTGTTACACGGTTTCATCTGATGGATAGTGCATCGA 660
QY 667 GACATCAAGCCTGAGAACATTTCTGTTGACCCACAGGACACATCAAGCTGTTGATTTT 726
Db 661 GACATCAAGCCTGAGAACATTTCTGTTGACCCACAGGACACATCAAGCTGTTGATTTT 720
QY 727 GATCTGCGCGGAAATGATTTCAACACAGATGTTGAATGCCAATCTCCGATTTGGGACC 786
Db 721 GATCTGCGCGGAAATGATTTCAACACAGATGTTGAATGCCAATCTCCGATTTGGGACC 780
QY 787 CCAGATTACATGGCTCCTGAGTGTGCTGATGTAAGGAGGAGTGGAAAGGACCTAC 846
Db 781 CCAGATTACATGGCTCCTGAGTGTGCTGATGTAAGGAGGAGTGGAAAGGACCTAC 840
QY 847 GGCCTGGACTGTGCTGTTGGCTGATGGCGGTGATTCCTATGAGATGATTTATGGGAGA 906
Db 841 GGCCTGGACTGTGCTGTTGGCTGATGGCGGTGATTCCTATGAGATGATTTATGGGAGA 900
QY 907 TCCCCCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAAATATGAAATTTCCAGGGG 966
Db 901 TCCCCCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAAATATGAAATTTCCAGGGG 960
QY 967 TTTTGAATTTCCAGATGACCCCAAGTGGAGAGTGTGCTGTTGATGATGATTTCAAAAGC 1026
Db 961 TTTTGAATTTCCAGATGACCCCAAGTGGAGAGTGTGCTGTTGATGATGATTTCAAAAGC 1020
QY 1027 TTGTTGCGGCGCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC 1086
Db 1021 TTGTTGCGGCGCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC 1080
QY 1087 TCTAAATTTGACTGGAAACAACTTCGTAACTCTCTCCCTCCCTTCCTGCCACCTCAAG 1146
Db 1081 TCTAAATTTGACTGGAAACAACTTCGTAACTCTCTCCCTCCCTTCCTGCCACCTCAAG 1140
QY 1147 TCGAGATGACACCTCCAAATTTGATGAAACAGAGAGAAATTCGTGGGTTTCATCTCT 1206
Db 1141 TCTGAGATGACACCTCCAAATTTGATGAAACAGAGAGAAATTCGTGGGTTTCATCTCT 1200
QY 1207 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTCCGCTTTTGGGGTTTTCG 1266
Db 1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTCCGCTTTTGGGGTTTTCG 1260
QY 1267 TACAGCAAGGACTGGGGATTTCTGTTAGATCTGAGTCTGTTGTTGGGTTGAGCTCC 1326
Db 1261 TACAGCAAGGACTGGGGATTTCTGTTAGATCTGAGTCTGTTGTTGGGTTGAGCTCC 1320
QY 1327 CTTGCCAAGACTAGCTCCATGTAAGAAAGAACTTCTCATCAAAAGCAAGAGTCAAGAC 1386
Db 1321 CTTGCCAAGACTAGCTCCATGTAAGAAAGAACTTCTCATCAAAAGCAAGAGTCAAGAC 1380
QY 1387 TCTCAGCAAGTGTCAAGGT 1409
Db 1381 TCTCAGCAAGTGTCAAGAT 1403

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RESULT 10

```

US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fziddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946

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; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-1

Query Match          92.3%; Score 1398.2; DB 18; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTGAAGTTCAAAATATGGAGCGCGAATCTCTTTGGATGCTGCTGCTGCTGAACCAATT 66
Db 1 ATGTGAAGTTCAAAATATGGAGCGCGAATCTCTTTGGATGCTGCTGCTGCTGCTGAACCAATT 60
QY 67 GCCAACCGGGCTCCAGGCTGATCTGTTCTTCCAGGGGAAACCCACCTTTATGACTCAA 126
Db 61 GCCAGCGGGCTCCAGGCTGATCTGTTCTTCCAGGGGAAACCCACCTTTATGACTCAA 120
QY 127 CAGCAGATGCTCTCTCTTTCCGAGAGGAGATATTAGATGCTGCTCTTTCTCTTTGAA 186
Db 121 CAGCAGATGCTCTCTCTTTCCGAGAGGAGATATTAGATGCTGCTCTTTCTCTTTGAA 180
QY 187 GAATGACGCTGCTGCTGCTGATGAAGATTAAGCAGCTGAGCAATCTTCTCGGAGATAT 246
Db 181 GAATGACGCTGCTGCTGCTGATGAAGATTAAGCAGCTGAGCAATCTTCTCGGAGATAT 240
QY 247 TCCGACACCACTAGCTGAGTTACAGAGAGCTCCAGCTTTCCGCAAAAGGACTTTCGAAGTCAGA 306
Db 241 TCCGACACCACTAGCTGAGTTACAGAGAGCTCCAGCTTTCCGCAAAAGGACTTTCGAAGTCAGA 300
QY 307 AGTCTTGTAGTGTGCTGCTCTTTGCTGAAAGTGCAGTGTGTAAGAGAGAAAGCAACCGGG 366
Db 301 AGTCTTGTAGTGTGCTGCTCTTTGCTGAAAGTGCAGTGTGTAAGAGAGAAAGCAACCGGG 360
QY 367 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCCGAGGAGAGTTTCA 426
Db 361 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCCGAGGAGAGTTTCA 420
QY 427 TTTTGGAGAGAGCGGAAACATATTATCTCGAAGCAAGCCCGTGGATGCCCAATTA 486
Db 421 TTTTGGAGAGAGCGGAAACATATTATCTCGAAGCAAGCCCGTGGATGCCCAATTA 480
QY 487 CAGTATGCTCTTTCAGGACAAATACCTTTATCTGCTCATGGAATATCAGCTGAGGG 546
Db 481 CAGTATGCTCTTTCAGGACAAATACCTTTATCTGCTCATGGAATATCAGCTGAGGG 540
QY 547 GACTTGTGCTGCTGCTTTGATATGAGGACAGTGTAGATGAAACCTGTATACAGTTT 606
Db 541 GACTTGTGCTGCTGCTTTGATATGAGGACAGTGTAGATGAAACCTGTATACAGTTT 600
QY 607 TACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCTGATGGATACCTGATCGA 666
Db 601 TACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCTGATGGATACCTGATCGA 660
QY 667 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
Db 661 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720
QY 727 GATCTGCGCGGAAATGAAATTCAAACAGATGCTGATGAAAGGAGTGGAAAGGACCTAC 786
Db 721 GATCTGCGCGGAAATGAAATTCAAACAGATGCTGATGAAAGGAGTGGAAAGGACCTAC 780
QY 787 CCAGATTACATGCTCTGCTGAGTGTGCTGATGTAAGGAGTGGAAAGGACCTAC 846
Db 781 CCAGATTACATGCTCTGCTGAGTGTGCTGATGTAAGGAGTGGAAAGGACCTAC 840
QY 847 GGCCTGAGCTGCTGCTGAGTGTGCTGAGTGGGCTGATTCCTATGAGATGATTTATGGGAGA 906

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Db      841  GGCTGGACTGTGACTGGTGGTCAAGTGGCGTGAATGCCCTATGAGATGATTTATGGGAGA  900
Qy      907  TCCCTCTTCGACAGAGGAACTCTGCGAGAACCTTCAATAAACAATATGATTTCCAGCGG  966
Db      901  TCCCTCTTCGACAGAGGAACTCTGCGAGAACCTTCAATAAACAATATGATTTCCAGCGG  960
Qy      967  TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTCTTGTGATCTGATTTCAAAGC  1026
Db      961  TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTCTTGTGATCTGATTTCAAAGC  1020
Qy      1027  TTCTGTGGCGGCGAGAAAGAGACTGAAGTTTGAAGGCTTTGCTGCCATCCTTTCTTC  1086
Db      1021  TTCTGTGGCGGCGAGAAAGAGACTGAAGTTTGAAGGCTTTGCTGCCATCCTTTCTTC  1080
Qy      1087  TCTAAATTTGACTGGAAACCAATTCGTAACTCTCTCCGCCCTTCGTTCCCACTCAAG  1146
Db      1081  TCTAAATTTGACTGGAAACCAATTCGTAACTCTCTCCGCCCTTCGTTCCCACTCAAG  1140
Qy      1147  TCCGAGATGACACCTCCATTTTGAATGAACAGAGAAATTCGTGGGTTTCATCTCT  1206
Db      1141  TCTGAGATGACACCTCCATTTTGAATGAACAGAGAAATTCGTGGGTTTCATCTCT  1200
Qy      1207  CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTCG  1266
Db      1201  CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTCG  1260
Qy      1267  TACAGACGACCTGGGATCTTGTAGATCTGATCTGATCTGATCTGATCTGATCTG  1326
Db      1261  TACAGACGACCTGGGATCTTGTAGATCTGATCTGATCTGATCTGATCTGATCTG  1320
Qy      1327  CCGTGCAGCTGAGCTCCATGGAAGAAACTTCTCAATCAAGCAAGAGAGCTACAAGAC  1386
Db      1321  CCGTGCAGCTGAGCTCCATGGAAGAAACTTCTCAATCAAGCAAGAGAGCTACAAGAC  1380
Qy      1387  TCTCAGCAAGTGTCAAGGT  1409
Db      1381  TCTCAGCAAGTGTCAAGAT  1403

RESULT 11
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prod
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-5701
; CURRENT APPLICATION NUMBER: US/10/017,216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match 92.3%; Score 1397.8; DB 13; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GGGGAGATGTTGAAGTTCAATATGAGCGGGAATCCCTTTGGATGCTGGTCTGCTGAA  60
Db      13  GGGGAGATGTTGAAGTTCAATATGAGCGGGAATCCCTTTGGATGCTGGTCTGCTGAA  72
Qy      61  CCAATGCCAACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATG  120
Db      73  CCAATGCCAGCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATG  132
Qy      121  ACTCAACACAGATGTCCTCTTCTCCGAGAGGAGATATAGATGCGCTCTTTGTTCTC  180

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Db      133  ACTCAACACAGATGTCCTCTCTTCCGAGAGGATATAGATGCGCTCTTTGTTCTC  192
Qy      181  TTTGAAGATCGAGTCAGCTGCTCTGATGAAGATTAAGACGAGTGAACATTTGTCCGG  240
Db      193  TTTGAAGATCGAGTCAGCTGCTCTGATGAAGATTAAGACGAGTGAACATTTGTCCGG  252
Qy      241  AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCCTTCGGAAGAGCTTCGAA  300
Db      253  AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCCTTCGGAAGAGCTTCGAA  312
Qy      301  GTCAGAGCTCTTGTAGGTTGTGCTCACTTGTCTGAAAGTGAAGTGAAGAGAAAGCA  360
Db      313  GTCAGAGCTCTTGTAGGTTGTGCTCACTTGTCTGAAAGTGAAGTGAAGAGAAAGCA  372
Qy      361  ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGAGCAG  420
Db      373  ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGAGCAG  432
Qy      421  GTTTCAATTTTGAAGAGAGCGGAACATATTTCTCGAAGCAACAAGCCGTGATCCCC  480
Db      433  GTTTCAATTTTGAAGAGAGCGGAACATATTTCTCGAAGCAACAAGCCGTGATCCCC  492
Qy      481  CAATTACAGTATGCTTTTTCAGGACAAATCACCTTTATCTGGTCATGGATATCAGCCT  540
Db      493  CAATTACAGTATGCTTTTTCAGGACAAATCACCTTTATCTGGTCATGGATATCAGCCT  552
Qy      541  GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTGTGATGATA  600
Db      553  GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTGTGATGATA  612
Qy      601  CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTCATCTGATGGGATACGTG  660
Db      613  CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTCATCTGATGGGATACGTG  672
Qy      661  CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGT  720
Db      673  CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGT  732
Qy      721  GATTTTGGATCTGCGCGAAATGAATTTCAAAAGATGTTGAATGCCAAACTCCCGATT  780
Db      733  GATTTTGGATCTGCGCGAAATGAATTTCAAAAGATGTTGAATGCCAAACTCCCGATT  792
Qy      781  GGGACCCCGAGTATACATGCTGCTGAGTCTGCTGATGCTGATGACGGGATGGAAGGC  840
Db      793  GGGACCCCGAGTATACATGCTGCTGAGTCTGCTGATGCTGATGACGGGATGGAAGGC  852
Qy      841  ACCTACGGCCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  900
Db      853  ACCTACGGCCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  912
Qy      901  GGGAGATCCCCCTTCGAGAGGGAACCTCTGCCAGAACCTTCAATTAACATTTGAATTC  960
Db      913  GGGAGATCCCCCTTCGAGAGGGAACCTCTGCCAGAACCTTCAATTAACATTTGAATTC  972
Qy      961  CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT  1020
Db      973  CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT  1032
Qy      1021  CAAAGCTTTGTTGGCGGCGAGAGAGAGAGCTGAAGTGTGAAGGCTCTTCTGCTGCATCT  1080
Db      1033  CAAAGCTTTGTTGGCGGCGAGAGAGAGAGCTGAAGTGTGAAGGCTCTTCTGCTGCATCT  1092
Qy      1081  TTCTTCTCTAAATTTGACTGGAAACCAATTCGTAACCTCTCTCCCGCTTTCGTTCCACC  1140
Db      1093  TTCTTCTCTAAATTTGACTGGAAACCAATTCGTAACCTCTCTCCCGCTTTCGTTCCACC  1152
Qy      1141  CTCAGTCCGACGATGACACCTCCAAATTTTGTATGAACAGAGAGAAATTCGTGGTTCA  1200
Db      1153  CTCAGTCCGACGATGACACCTCCAAATTTTGTATGAACAGAGAGAAATTCGTGGTTCA  1212
Qy      1201  TCCTCTCGGTCGACGCTGAGCCCTCAGGCTTCTCGGTTGAAAGCTGCGGTTTGTGGG  1260

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Db 1213 TCCTCTCCGTCCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTGCCCGTTTGTGGG 1272

Qy 1261 TTTTCGTACACCAAGCACTGGGATCTTGTGTAGATCTGAGTCTGTGTGTGGGTCTG 1320

Db 1273 TTTTCGTACACCAAGCACTGGGATCTTGTGTAGATCTGAGTCTGTGTGTGGGTCTG 1332

Qy 1321 GACTCCCTGCCAAGACTAGCTTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1380

Db 1333 GACTCCCTGCCAAGACTAGCTTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1392

Qy 1381 CAAGACTCTCAGGACAAGTGTCAAGGT 1409

Db 1393 CAAGACTCTCAGGACAAGTGTCAAGAT 1421

RESULT 12

US-10-325-430-10

/ Sequence 10, Application US/10325430

/ Publication No. US20030153525A1

/ GENERAL INFORMATION:

/ APPLICANT: Millennium Pharmaceuticals, Inc

/ APPLICANT: Silos-Santiago, Inmaculada

/ APPLICANT: Rosenfeld, Julie Beth

/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,

/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,

/ FILE OF INVENTION: 32838, 336 and 52908

/ FILE REFERENCE: MP101-294P1RNM

/ CURRENT APPLICATION NUMBER: US/10/325,430

/ CURRENT FILING DATE: 2002-12-19

/ PRIOR APPLICATION NUMBER: US 60/341,953

/ PRIOR FILING DATE: 2001-12-19

/ NUMBER OF SEQ ID NOS: 21

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 10

/ TYPE: DNA

/ ORGANISM: Homo Sapiens

US-10-325-430-10

Query Match 92.3%; Score 1397.8; DB 15; Length 6574;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGAGATGTTGAAGTCAATATATGAGCGCGGAATCCTTTGGATGCTGTGCTGCTGAA 60

Db 13 GGGAGATGTTGAAGTCAATATATGAGCGCGGAATCCTTTGGATGCTGTGCTGCTGAA 72

Qy 61 CCATTGCAACCGGCTCCAGGCTGAATCTGTTTCCAGGCGGAACCAACCTTTATG 120

Db 73 CCATTGCAACCGGCTCCAGGCTGAATCTGTTTCCAGGCGGAACCAACCTTTATG 132

Qy 121 ACTCAACAGCATCTCTCTTCCAGGAGGATATAGATGCCCTCTTTGTTCTC 180

Db 133 ACTCAACAGCATCTCTCTTCCAGGAGGATATAGATGCCCTCTTTGTTCTC 192

Qy 181 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTCAGCACTTTGTCGG 240

Db 193 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTCAGCACTTTGTCGG 252

Qy 241 AGTATTCGACACCATAGCTGAGTACAGGCTCCAGGCTTCCGCAAGGACTTCGAA 300

Db 253 AGTATTCGACACCATAGCTGAGTACAGGCTCCAGGCTTCCGCAAGGACTTCGAA 312

Qy 301 GTCAGAGTCTGTAGGTTGTGTCACCTTGTGAGTGCAGGTGTTAAGAGAGAGCA 360

Db 313 GTCAGAGTCTGTAGGTTGTGTCACCTTGTGAGTGCAGGTGTTAAGAGAGAGCA 372

Qy 361 ACCGGGACATCTATGCTATGAAGATGAAGAGGCTTTATTTGGCCAGGAGAG 420

Db 373 ACCGGGACATCTATGCTATGAAGATGAAGAGGCTTTATTTGGCCAGGAGAG 432

Qy 421 GTTTCATTTTGGAGAGAGCGGAACATATATCTCGAAGCAAGCCGCTGGATCCC 480

Db 433 GTTTCATTTTTCGAGAGAGCGGAACATATATCTCGAAGCAAGCCCGTGGATCCCC 492

Qy 481 CAATTACAGTATGCTTTTCAGGACAAAATCACTTTTATCTGTCATCGAATATCAGCT 540

Db 493 CAATTACAGTATGCTTTTCAGGACAAAATCACTTTTATCTGTCATCGAATATCAGCT 552

Qy 541 GGAGGGAGCTTCTGTCACCTTTTGAATAGATAGAGGACCACTTAGATGAAAACCTGATA 600

Db 553 GGAGGGAGCTTCTGTCACCTTTTGAATAGATAGAGGACCACTTAGATGAAAACCTGATA 612

Qy 601 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTG 660

Db 613 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTG 672

Qy 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGTGTGTG 720

Db 673 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGTGTGTG 732

Qy 721 GATTTGGATCTGCCCGGAAAATGAATTCAAAACAGATGTTGAATGCCAACTCCGATTT 780

Db 733 GATTTGGATCTGCCCGGAAAATGAATTCAAAACAGATGTTGAATGCCAACTCCGATTT 792

Qy 781 GGGACCCAGATTTACATGCTCTCTGAAAGTCTGACTGTGATCAACGGGATGAAAAGGC 840

Db 793 GGGACCCAGATTTACATGCTCTCTGAAAGTCTGACTGTGATCAACGGGATGAAAAGGC 852

Qy 841 ACTACGGCTGAGCTGTGACTGTGTTGTTGAGTGGGCTGATTTGCCATAGAGATGATTTAT 900

Db 853 ACTACGGCTGAGCTGTGACTGTGTTGTTGAGTGGGCTGATTTGCCATAGAGATGATTTAT 912

Qy 901 GGGAGATCTCCCTTCCAGAGGGAACCTCTGCAGAACCTTCAATAAATATGAATTC 960

Db 913 GGGAGATCTCCCTTCCAGAGGGAACCTCTGCAGAACCTTCAATAAATATGAATTC 972

Qy 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTTGTGATCTGATTT 1020

Db 973 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTTGTGATCTGATTT 1032

Qy 1021 CAAGCTTTTGTGCGGCGAAGAGAGACTGAAGTTTGAAGGTTTTCCTGCTGCCATCCT 1080

Db 1033 CAAGCTTTTGTGCGGCGAAGAGAGACTGAAGTTTGAAGGTTTTCCTGCTGCCATCCT 1092

Qy 1081 TTCTTCTCTAAAATTTGACTTGAACCAATTCGTAATCTCTCTCCCTCCCTTCCTCCACC 1140

Db 1093 TTCTTCTCTAAAATTTGACTTGAACCAATTCGTAATCTCTCTCCCTCCCTTCCTCCACC 1152

Qy 1141 CTCAGTCCGACGATGACACTCCAAATTTTGAATGAACAGAGAAATTCGTGGGTTTCA 1200

Db 1153 CTCAGTCTGACGATGACACTCCAAATTTTGAATGAACAGAGAAATTCGTGGGTTTCA 1212

Qy 1201 TCCTCTCCGTGCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGCTTTGTGGGG 1260

Db 1213 TCCTCTCCGTGCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGCTTTGTGGGG 1272

Qy 1261 TTTTCGTACAGCAAGGCACTGGGATTTTGTGATCTGAGTCTGTTGTGTCGGGTCTG 1320

Db 1273 TTTTCGTACAGCAAGGCACTGGGATTTTGTGATCTGAGTCTGTTGTGTCGGGTCTG 1332

Qy 1321 GACTCCCTCCCAAGACTAGCTTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380

Db 1333 GACTCCCTCCCAAGACTAGCTTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392

Qy 1381 CAAGACTCTCAGGACAAGTGTCAAGGT 1409

Db 1393 CAAGACTCTCAGGACAAGTGTCAAGAT 1421

RESULT 13

US-10-757-262-51

/ Sequence 51, Application US/10757262

/ Publication No. US20040197825A1

/ GENERAL INFORMATION:

/ APPLICANT: Karicheti, Venkateswarlu

```
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)....(6180)
; US-10-757-262-51

Query Match      92.3%; Score 1397.8; DB 18; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1  GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCCCTTGGATGCTGCTGCTGAA 60
DB      13  GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCCCTTGGATGCTGCTGCTGAA 72
QY      61  CCCATTGCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120
DB      73  CCCATTGCCAGCGCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 132
QY     121  ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 180
DB     133  ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 192
QY     181  TTTGAAGAATGCACTGCTGCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 240
DB     193  TTTGAAGAATGCACTGCTGCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 252
QY     241  AAGTATTTCCGACACCAATAGTGTAGTGTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAA 300
DB     253  AAGTATTTCCGACACCAATAGTGTAGTGTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAA 312
QY     301  GTCAAGAGCTTCTAGTGTGTGCTCACTTTGCTGAAGTGCAGTGTGTAGAGGAAGCA 360
DB     313  GTCAAGAGCTTCTAGTGTGTGCTCACTTTGCTGAAGTGCAGTGTGTAGAGGAAGCA 372

361  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCGAGAGCAG 420
DB      373  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCGAGAGCAG 432
QY      421  GTTTCATTTTGGAGGAGAGCGGAAACATATTATCTGAAAGCACAAGCCCGTGTGATCCCC 480
DB      433  GTTTCATTTTGGAGGAGAGCGGAAACATATTATCTGAAAGCACAAGCCCGTGTGATCCCC 492
QY      481  CAATTTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGATATCAGCCT 540
DB      493  CAATTTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGATATCAGCCT 552
QY      541  GAGGGGACTTGTCTGTCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGATA 600
DB      553  GAGGGGACTTGTCTGTCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGATA 612
QY      601  CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTACAGCGTTTCACTGTATGGGATACGTG 660
DB      613  CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTACAGCGTTTCACTGTATGGGATACGTG 672
QY      661  CATCGAGACATCAAGCCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720
DB      673  CATCGAGACATCAAGCCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 732
QY      721  GATTTTGGATCTGCGCGGAAAATGAATTCAAACAAAGATGTGAATGCCAACTCCCGATT 780
DB      733  GATTTTGGATCTGCGCGGAAAATGAATTCAAACAAAGATGTGAATGCCAACTCCCGATT 792
QY      781  GGGACCCCGAGATATACATGGCTCCCTGAAGTGTGCTGACTGTGATGAACGGGGATGGAAGGC 840
DB      793  GGGACCCCGAGATATACATGGCTCCCTGAAGTGTGCTGACTGTGATGAACGGGGATGGAAGGC 852
QY      841  ACCTACGGCTTGGACTGTGACTGTGCTGAGTGGGCGTGTGCTATGATGATGATTTAT 900
DB      853  ACCTACGGCTTGGACTGTGACTGTGCTGAGTGGGCGTGTGCTATGATGATGATTTAT 912
QY      901  GGGAGATCCCCCTTGGCAGAGAGGAACTCTGCCAGAACCTCTGCAGAACCTTCAATATGAAATTC 960
DB      913  GGGAGATCCCCCTTGGCAGAGAGGAACTCTGCAGAACCTTCTGCAGAACCTTCAATATGAAATTC 972
QY      961  CAGCGGTTTTTGAATTTTCAGATGACCCCCAAAGTGTGAGTGTGCTGCTGCTGCT 1020
DB      973  CAGCGGTTTTTGAATTTTCAGATGACCCCCAAAGTGTGAGTGTGCTGCTGCTGCT 1032
QY     1021  CAAAGCTTGTGTCGGCGCAGAAAGAGAGACTGAAAGTTTGAAGTGTGCTGCTGCTGCT 1080
DB     1033  CAAAGCTTGTGTCGGCGCAGAAAGAGAGACTGAAAGTTTGAAGTGTGCTGCTGCTGCT 1092
QY     1081  TTCTTCTCTAAATTTGACTGGAAACAAATTCGTAACCTCTCTCCCGCCCTTCTGTTCCACCC 1140
DB     1093  TTCTTCTCTAAATTTGACTGGAAACAAATTCGTAACCTCTCTCCCGCCCTTCTGTTCCACCC 1152
QY     1141  CTCAGTCCGACGATGACACTCCCAATTTTGAATGAACAGAGAGAAATTCGTTGGTTTCA 1200
DB     1153  CTCAGTCCGACGATGACACTCCCAATTTTGAATGAACAGAGAGAAATTCGTTGGTTTCA 1212
QY     1201  TCCTCTCCGTCGACGTCGAGCCCTCAGGCTTCTCGGGTGAAGAACTTCGCGTTTGTGGGG 1260
DB     1213  TCCTCTCCGTCGACGTCGAGCCCTCAGGCTTCTCGGGTGAAGAACTTCGCGTTTGTGGGG 1272
QY     1261  TTTTCGTACAGCAAGGCACTGGGGATTTCTGGTGTAGTCTGAGTGTGTGTGTCGGGCTG 1320
DB     1273  TTTTCGTACAGCAAGGCACTGGGGATTTCTGGTGTAGTCTGAGTGTGTGTGTCGGGCTG 1332
QY     1321  GACTCCCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGAGCTA 1380
DB     1333  GACTCCCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGAGCTA 1392
QY     1381  CAAGACTCTCAGGACAAAGTGTCAAGGT 1409
DB     1393  CAAGACTCTCAGGACAAAGTGTCAAGAT 1421
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; NAME/KEY: CDS									
; LOCATION: (1)....(6162)									
Us-10-325-430-11									
Query Match									
Best Local Similarity 91.98; Score 1391.8; DB 15; Length 6162;									
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
Qy	7	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTGCTGCTGAACCCATT	66						
Db	1	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTGCTGCTGAACCCATT	60						
Qy	67	GCCAAACCGGCTCCAGCGTGAATCTGTTCTTCAGGGGAAACCAACCCCTTATGACTCAA	126						
Db	61	GCCAGCGGCGCTCCAGCGTGAATCTGTTCTTCAGGGGAAACCAACCCCTTATGACTCAA	120						
Qy	127	CAGCAGATGCTCCTCTTTCCGAGAGGGATATTAGATGCCCTCTTGTCTCTTTGAA	186						
Db	121	CAGCAGATGCTCCTCTTTCCGAGAGGGATATTAGATGCCCTCTTGTCTCTTTGAA	180						
Qy	187	GAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCCGGAAGTAT	246						
Db	181	GAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCCGGAAGTAT	240						
Qy	247	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGGCTTCGSCAAAGGACTTCGAACTCAGA	306						
Db	241	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGGCTTCGSCAAAGGACTTCGAACTCAGA	300						
Qy	307	AGTCTTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAAAGCAACCGGG	366						
Db	301	AGTCTTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAAAGCAACCGGG	360						
Qy	367	GACATCTATGCTATGAAGTGAAGAGAAAGCTTTATTTGGCCAGGAGCAGGTTTCA	426						
Db	361	GACATCTATGCTATGAAGTGAAGAGAAAGCTTTATTTGGCCAGGAGCAGGTTTCA	420						
Qy	427	TTTTTTTCAGGAAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA	486						
Db	421	TTTTTTTCAGGAAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA	480						
Qy	487	CAGTATGCCCTTTTCAGGACAAAATACACCTTTATCTGGTCAATGGAATATCAGCCTGGAGG	546						
Db	481	CAGTATGCCCTTTTCAGGACAAAATACACCTTTATCTGGTCAATGGAATATCAGCCTGGAGG	540						
Qy	547	GACTTGTCTGTCACTTTTGAATAGATATGAGGACAGCTTAGATGAAAACCTGATACAGTTT	606						
Db	541	GACTTGTCTGTCACTTTTGAATAGATATGAGGACAGCTTAGATGAAAACCTGATACAGTTT	600						
Qy	607	TACCTAGCTGAGTGTATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTGCATCGA	666						
Db	601	TACCTAGCTGAGTGTATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTGCATCGA	660						
Qy	667	GACATCAAGCCTGAGAAACATCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	726						
Db	661	GACATCAAGCCTGAGAAACATCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	720						
Qy	727	GGATCTCCCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTGGGACC	786						
Db	721	GGATCTCCCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTGGGACC	780						
Qy	787	CCAGATTACATGGCTCCTGAAAGTGTGACTGTGATGAACCGGGATGGAAGGACCTTAC	846						
Db	781	CCAGATTACATGGCTCCTGAAAGTGTGACTGTGATGAACCGGGATGGAAGGACCTTAC	840						
Qy	847	GGCCTGACCTGTGACTGGTGTGCTGGGCGTGAATGCCCTATGAGATGATTTATGGAGA	906						
Db	841	GGCCTGACCTGTGACTGGTGTGCTGGGCGTGAATGCCCTATGAGATGATTTATGGAGA	900						
Qy	907	TCCCCCTTCGAGAGGAAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG	966						
Db	901	TCCCCCTTCGAGAGGAAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG	960						
Qy	967	TTTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC	1026						

Search completed: November 8, 2004, 10:40:20  
Job time : 778 secs

Db	961	TTTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTCATAAAGC	1020
Qy	1027	TTGTTGTGCGGCCGAGAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC	1086
Db	1021	TTGTTGTGCGGCCGAGAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC	1080
Qy	1087	TCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCCCCCTTCGTTCCACCCCTCAAG	1146
Db	1081	TCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCCCCCTTCGTTCCACCCCTCAAG	1140
Qy	1147	TCCGACGATGACACCTCCAAATTTTGATGAACGAGAGAGAAATTCGTGGGTTTCATCTCT	1206
Db	1141	TCTGACGATGACACCTCCAAATTTTGATGAACGAGAGAGAAATTCGTGGGTTTCATCTCT	1200
Qy	1207	CGTCCCAAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCG	1266
Db	1201	CGTCCCAAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCG	1260
Qy	1267	TACACAAAGGCACTGGGGAATCTTGGTAGATCTGAGTCTGTGTGTGCGGTTCTGGACTCC	1326
Db	1261	TACACAAAGGCACTGGGGAATCTTGGTAGATCTGAGTCTGTGTGTGCGGTTCTGGACTCC	1320
Qy	1327	CCTGCCAAGACTAGCTCCATGGAAGAACTTCTCTCATCAAAAGCAAGAGCTACAAGAC	1386
Db	1321	CCTGCCAAGACTAGCTCCATGGAAGAACTTCTCTCATCAAAAGCAAGAGCTACAAGAC	1380
Qy	1387	TCTCAGGACAAAGTGTCACAAGGT	1409
Db	1381	TCTCAGGACAAAGTGTCACAAGAT	1403

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: November 8, 2004, 01:59:29 ; Search time 726 Seconds  
(without alignments)  
10954.370 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 GGGAGATGTTGAAGTCAA.....TCTGAGCGCGCGATCGCTGA 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues  
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_23Sep04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	100.0	1515	8 ACA61394	ACA61394 cDNA enco
2	1515	100.0	1515	10 AAD59938	Aad59938 Human kin
3	1515	100.0	1515	12 ADO40591	Ado40591 Human kin
4	1510.2	99.7	2066	6 AAD26454	Aad26454 Human kin
5	1505.8	99.4	1765	10 AB268726	Ab268726 Nucleotid
6	1481.8	97.8	1485	10 AB268725	Ab268725 Nucleotid
7	1404.2	92.7	6298	6 AAD38864	Aad38864 Human kin
8	1398.2	92.3	1870	8 ADA05643	Ada05643 Human NOV
9	1398.2	92.3	5877	6 ABQ78871	Abq78871 Human kin
10	1398.2	92.3	6156	9 AAL55217	Aal55217 Human CRI
11	1398.2	92.3	6165	6 ABQ78870	Abq78870 Human kin
12	1398.2	92.3	6165	9 AAL55214	Aal55214 Human CRI
13	1398.2	92.3	8603	6 AAL55215	Aal55215 Human CRI
14	1397.8	92.3	6574	6 AAD39191	Aad39191 Human MDP
15	1397.8	92.3	6574	10 ADF60992	Adf60992 Pain asso
16	1395	92.1	1870	12 AAD62808	Aad62808 Human NOV
17	1391.8	91.9	6162	10 ADF60993	Adf60993 ORF of pa
18	1388	91.6	8656	12 AAD96544	Adi96544 Human cit
19	1382	91.2	6159	4 AAS06701	Aas06701 Polynucle
20	1375.8	90.8	6189	6 ABS83436	Abs83436 RBC/RAC-i
21	1375.8	90.8	6189	8 ADA05641	Ada05641 Human NOV

22	1375.8	90.8	6189	12 ADN62806	Adn62806 Human NOV
23	1375.8	90.8	6201	6 ABS63435	Abs63435 Human cDN
24	1375.8	90.8	6201	8 ADA05653	Ada05653 Human NOV
25	1375.8	90.8	6201	12 ADN62818	Adn62818 Human NOV
26	1158	76.4	2380	10 AB268776	Ab268776 Nucleotid
27	963.2	63.6	2162	8 ABX71191	Abx71191 Novel hum
28	955.4	63.1	957	11 ADN62729	Adn62729 Human cit
29	940.8	62.1	1048	5 AAS79753	Aas79753 DNA encod
30	760.8	50.2	1133	10 ADJ79946	Adj79946 Human kin
31	578.8	38.2	2896	5 ABV30132	Abv30132 Human pro
32	441.8	25.2	446	5 ABV15823	Abv15823 Human pro
33	434.4	28.7	485	5 ABV45624	Abv45624 Human pro
34	247.2	16.3	3835	8 ABT33346	Abt33346 NOX DNA
35	247.2	16.3	3985	8 ABT33347	Abt33347 NOX DNA
36	246.8	16.3	1530	6 AAD38845	Aad38845 Human kin
37	246.8	16.3	4698	12 ADP47966	Adp47966 Human MRC
38	246.8	16.3	4707	12 ADP95101	Adp95101 Human ser
39	246.8	16.3	4944	12 ADF95099	Adf95099 Human ser
40	246.8	16.3	5373	6 AAD30567	Aad30567 Human kin
41	246.8	16.3	5438	12 ADJ96545	Adj96545 Human dys
42	246.8	16.3	5619	12 ADI40903	Adi40903 Human kin
43	246.8	16.3	5973	10 ADC99116	Adc99116 Human KPP
44	238.8	15.8	5373	12 ADP47970	Adp47970 Human PKI
45	236.8	15.6	5094	12 ADK71883	Adk71883 Human kin

ALIGNMENTS

RESULT 1  
ACA61394  
ID ACA61394 standard; cDNA; 1515 BP.  
XX  
AC ACA61394;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE cDNA encoding novel human kinase.  
XX  
KW Human; ss; gene; gene therapy; kinase; antisense.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 5'UTR 1..6 /\*tag= a  
FT CDS 7..1500 /\*tag= b  
FT FT /product= "Kinase"  
FT 3'UTR 1501..1515 /\*tag= c  
XX  
US2003022340-A1.  
PN 30-JAN-2003.  
XX  
XX 11-SEP-2002; 2002US-00238709.  
XX  
XX 13-MAR-2001; 2001US-00804471.  
XX  
XX (APPL-) APPLERA CORP.  
XX Webster M, Yan C, Di Francesco V, Beasley EM;  
XX WPI; 2003-438978/41.  
XX P-PSDB; ABU10126.  
XX  
XX New human kinase peptides useful as models or targets for the development  
XX of therapeutic agents that modulate kinase activity, for eliciting immune  
XX response, and in identifying compounds that modulate kinase activity or  
XX expression.  
XX Claim 4; Fig 1; 207pp; English.  
PS









QY 1381 CAAGACTCTCAGGACAAAGTGTCAAGGATATTTATTTCCGACGGCGCTCTCTCTTGC 1440  
 Db 1381 CAAGACTCTCAGGACAAAGTGTCAAGGATATTTATTTCCGACGGCGCTCTCTCTTGC 1440

QY 1441 TCAGGATCTCCCGTCCGCTATATGCAAGGATCCGCGCGCGCTGCTGCTCTGA 1500  
 Db 1441 TCAGGATCTCCCGTCCGCTATATGCAAGGATCCGCGCGCGCTGCTGCTCTGA 1500

QY 1501 GCGGCTGATCCGTA 1515  
 Db 1501 GCGGCTGATCCGTA 1515

RESULT 3  
 ADO40591  
 ID ADO40591 standard; cDNA; 1515 BP.  
 AC ADO40591;  
 XX 29-JUL-2004 (first entry)  
 DT Human kinase cDNA.  
 XX Kinase; rho/rae-interacting citron kinase; drug screening;  
 KW Kinase related disorder; human; chromosome 12; gene; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1..6  
 FT 5'UTR /\*tag= a  
 FT CDS 7..1500  
 FT /\*tag= b  
 FT /\*product= "Human kinase protein"  
 FT 3'UTR 1501..1515  
 FT /\*tag= c  
 XX US2004091993-A1.  
 XX 13-MAY-2004.  
 XX 02-DEC-2003; 2003US-00724594.  
 XX 13-MAR-2001; 2001US-00804471.  
 XX 11-SEP-2002; 2002US-00238709.  
 XX (APPL-) APPLERA CORP.  
 XX Webster M, Yan C, Di Francesco V, Beasley EM;  
 XX WPI; 2004-374957/35.  
 XX P-PSDB; ADO40592.  
 XX New isolated human kinase proteins and nucleic acids, useful for  
 PT developing human therapeutic targets, identifying therapeutic proteins or  
 PT serve as targets for the development of human therapeutic agents that  
 PT modulate kinase activity.  
 XX Claim 4; SEQ ID NO 1; 207pp; English.  
 XX The present invention provides a kinase polypeptide and its encoding  
 CC polynucleotide. The polypeptide and polynucleotide of the invention are  
 CC useful as models for the development of human therapeutic targets, aid in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents that modulate kinase activity in  
 CC cells and tissues that express the kinase. The invention is also useful  
 CC for biological assays related to kinases, in drug screening assays, for  
 CC treating disorders characterized by an absence of inappropriate and  
 CC unwanted expression of the protein. The present sequence is human kinase  
 CC cDNA. The human kinase gene is located on chromosome 12.  
 XX Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match 100.0%; Score 1515; DB 12; Length 1515;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGAAATCCCTTTGGATGCTGTGCTGTGAA 60  
 Db 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGAAATCCCTTTGGATGCTGTGCTGTGAA 60

QY 61 CCCATTCCCAACCGGCGCTCCAGGCTGAATCTCTTCTCCAGGGGAAACACACCTTTATG 120  
 Db 61 CCCATTCCCAACCGGCGCTCCAGGCTGAATCTCTTCTCCAGGGGAAACACACCTTTATG 120

QY 121 ACTCAACAGCAGATGTCCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTTGTCTC 180  
 Db 121 ACTCAACAGCAGATGTCCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTTGTCTC 180

QY 181 TTTGAAGAATGTCAGTCCAGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTTGTCGG 240  
 Db 181 TTTGAAGAATGTCAGTCCAGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTTGTCGG 240

QY 241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCGAAAGGACTTCGAA 300  
 Db 241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCGAAAGGACTTCGAA 300

QY 301 GTCAAGATCTTGTAGGTTGTGCTCACTTTGCTGAAGTGCAGGCTGTAGAGAGAAGCA 360  
 Db 301 GTCAAGATCTTGTAGGTTGTGCTCACTTTGCTGAAGTGCAGGCTGTAGAGAGAAGCA 360

QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAAAGAGGCTTTATTTGGCCCAAGAGCAG 420  
 Db 361 ACCGGGACATCTATGCTATGAAGTGAAGAAAGAGGCTTTATTTGGCCCAAGAGCAG 420

QY 421 GTTTCATTTTTGAGGAAGCGCGAACATATATCTCGAAGCACAAGCCCGTGGATCCCC 480  
 Db 421 GTTTCATTTTTGAGGAAGCGCGAACATATATCTCGAAGCACAAGCCCGTGGATCCCC 480

QY 481 CAATTACAGTATGCTTTTACAGGACAAAATCACTTTATCTGCTCATGGAATATCAGCCT 540  
 Db 481 CAATTACAGTATGCTTTTACAGGACAAAATCACTTTATCTGCTCATGGAATATCAGCCT 540

QY 541 GGAGGGACTTGTCTACCTTTTGAATAGATATGAGGACCAAGTATGATAAACCCTGATA 600  
 Db 541 GGAGGGACTTGTCTACCTTTTGAATAGATATGAGGACCAAGTATGATAAACCCTGATA 600

QY 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTACAGGCTTCTGATGGATACGCTG 660  
 Db 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTACAGGCTTCTGATGGATACGCTG 660

QY 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
 Db 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720

QY 721 GATTTGGATCTGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATT 780  
 Db 721 GATTTGGATCTGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATT 780

QY 781 GGGACCCAGATTACATGGCTCCTGAAAGTCTGCTGATGAACCGGGATGGAAAGGC 840  
 Db 781 GGGACCCAGATTACATGGCTCCTGAAAGTCTGCTGATGAACCGGGATGGAAAGGC 840

QY 841 ACCTACGGCTGAGCTGTGATGCTGGTGTGCTGGGCGTATTCCTCTATGAGATGATTAT 900  
 Db 841 ACCTACGGCTGAGCTGTGATGCTGGTGTGCTGGGCGTATTCCTCTATGAGATGATTAT 900

QY 901 GGGAGATCCCCCTTCGACAGAGGAACTCTGCGCAGAACCTTCAATAACATTATGAATTTC 960  
 Db 901 GGGAGATCCCCCTTCGACAGAGGAACTCTGCGCAGAACCTTCAATAACATTATGAATTTC 960

QY 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGAGTGAAGTCTTCTTGTGATT 1020  
 Db 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGAGTGAAGTCTTCTTGTGATT 1020



QY 301 GTGAGAGTCTTGTAGTGTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAAGCA 360  
 Db 308 GTCAAGAAGTCTTGTAGTGTGCTCACTTTGCTGAAGTGCAGGTGCTAAGAGAGAAAGCA 367  
 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAAGAGCTTTATTTGGCCCGCAGAGACAG 420  
 Db 368 ACCGGGACATCTATGCTATGAAGTGAAGAAGAGCTTTATTTGGCCCGCAGAGACAG 427  
 QY 421 GTTTTCATTTTTCAGGAGAGCGGAACATATTTCTCGAAGCAACAGCCGCTGGATCCCC 480  
 Db 428 GTTTTCATTTTTCAGGAGAGCGGAACATATTTCTCGAAGCAACAGCCGCTGGATCCCC 487  
 QY 481 CAATTAACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTATGGAATATCAGCCT 540  
 Db 488 CAATTAACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTATGGAATATCAGCCT 547  
 QY 541 GGAGGGGACTTGTGTGCTACCTTTTGAATAGATATGAGGACAGTATGATGAATAACCTGATA 600  
 Db 548 GGAGGGGACTTGTGTGCTACCTTTTGAATAGATATGAGGACAGTATGATGAATAACCTGATA 607  
 QY 601 CAGTTTTACCTAGTGTGAGTGAATTTGGCTGTTTCACAGCGTTCATCTGATGGATACGTG 660  
 Db 608 CAGTTTTACCTAGTGTGAGTGAATTTGGCTGTTTCACAGCGTTCATCTGATGGATACGTG 667  
 QY 661 CATCGAGACATCAAGCTGAGAACATCTCTGTTGACCGCACAGGACACATCAAGCTGTTG 720  
 Db 668 CATCGAGACATCAAGCTGAGAACATCTCTGTTGACCGCACAGGACACATCAAGCTGTTG 727  
 QY 721 GATTTTGGATCTCCGCGAAGAAATGAAATCAAAAGATGGTGAATGCCAAATCTCCCGATT 780  
 Db 728 GATTTTGGATCTCCGCGAAGAAATGAAATCAAAAGATGGTGAATGCCAAATCTCCCGATT 787  
 QY 781 GGGACCCACAGATTACATGCTCTCTGAGTGTGCTGATGAACGGGGATGGAAGAGC 840  
 Db 788 GGGACCCACAGATTACATGCTCTCTGAGTGTGCTGATGAACGGGGATGGAAGAGC 847  
 QY 841 ACCTACGGCTGACTGTGACTGTGCTGCTGAGTGGGCTGATTTGCTATGAGATGATTAT 900  
 Db 848 ACCTACGGCTGACTGTGACTGTGCTGAGTGGGCTGATTTGCTATGAGATGATTAT 907  
 QY 901 GGGAGATCTCCCTTCGAGAGGAACTCTGCGAGAACTTCAATAAATTTATGATTTTC 960  
 Db 908 GGGAGATCTCCCTTCGAGAGGAACTCTGCGAGAACTTCAATAAATTTATGATTTTC 967  
 QY 961 CAGCGGTTTTGAAATTTTCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATT 1020  
 Db 968 CAGCGGTTTTGAAATTTTCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATT 1027  
 QY 1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCT 1080  
 Db 1028 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCT 1087  
 QY 1081 TTCTTCTTAAATTTGACTGGAAACAATTCTGTAATCTCTCTCCCTTCTGTTCCCAAC 1140  
 Db 1088 TTCTTCTTAAATTTGACTGGAAACAATTCTGTAATCTCTCTCCCTTCTGTTCCCAAC 1147  
 QY 1141 CTCAGTTCGACCATGACACTCCCAATTTTGTATGACCAAGAGAAATTCGTTGGTTTCA 1200  
 Db 1148 CTCAGTTCGACCATGACACTCCCAATTTTGTATGACCAAGAGAAATTCGTTGGTTTCA 1207  
 QY 1201 TCCTCTCCGTCGAGTGAAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGG 1260  
 Db 1208 TCCTCTCCGTCGAGTGAAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGG 1267  
 QY 1261 TTTTCGTACAGGAGGACTGGGATCTTGTGATCTGAGTCTGTTGTTGTCGGGCTG 1320  
 Db 1268 TTTTCGTACAGGAGGACTGGGATCTTGTGATCTGAGTCTGTTGTTGTCGGGCTG 1327  
 QY 1321 GACTCCCTGCCAAGACTAGTCCATCGGAAAGAAATCTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1328 GACTCCCTGCCAAGACTAGTCCATCGGAAAGAAATCTCTCATCAAAAGCAAGAGCTA 1387

QY 1381 CAAGACTCTCAGGACAAAGTGTCAACAAGTATTTATTTCCGACGCGGCTCTCTTCCTTGC 1440  
 Db 1388 CAAGACTCTCAGGACAAAGTGTCAACAAGTATTTATTTCCGACGCGGCTCTCTTCCTTGC 1447  
 QY 1441 TCCAGGATCTCTCCGCTCCGTATATGTCCAAGGATTCGCCCCGGGCGCTGCTGCTGCTGA 1500  
 Db 1448 TCCAGGATCTCTCCGCTCCGTATATGTCCAAGGATTCGCCCCGGGCGCTGCTGCTGCTGA 1507  
 QY 1501 GCCGCTGATCCGTA 1515  
 Db 1508 GCCGCTGATCCGTA 1522

RESULT 5  
 ABZ68726  
 ID ABZ68726 standard; DNA; 1765 BP.  
 XX AC ABZ68726;  
 XX DT 16-MAY-2003 (first entry)  
 XX DE Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.  
 KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
 KW chronic obstructive pulmonary disease; hypertension; diabetes;  
 KW coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
 KW gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
 KW polycystic ovarian syndrome; fertility; depression; gene; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..1494  
 FT /\*tag= a  
 FT /product= "citron rho/rac-interacting kinase-short  
 XX kinase"  
 FN WO2003004629-A2.  
 XX PD 16-JAN-2003.  
 XX PF 01-JUL-2002; 2002WO-EP007229.  
 XX PR 02-JUL-2001; 2001US-0301853P.  
 PR 10-DEC-2001; 2001US-0337130P.  
 PR 25-APR-2002; 2002US-0375015P.  
 XX PA (FARB ) BAYER AG.  
 XX PI Zhu Z;  
 XX WPI; 2003-221595/21.  
 DR P-PSDB; ABP97687.  
 XX New human citron rho/rac-interacting kinase-short kinase polypeptide and  
 PT polynucleotide for preventing or treating diseases associated with the  
 PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
 PT disease.  
 XX Claim 1; Fig 18; 145pp; English.  
 CC The present sequence encodes a human citron rho/rac-interacting kinase-  
 CC short kinase polypeptide. The polynucleotide and polypeptide of the  
 CC invention are useful in preventing, ameliorating, or treating diseases  
 CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression

Accession	Species	Gene	Location/Qualifiers
D5	1027	TTTTTGAATTTCCAGATGACCCCAAGATGAGCAGTGCATCTTCTTGATCTGATTCAAGC	1027
QY	1027	TTGTTGTCGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTCTGCTGCCATCTTTCTTC	1086
DB	1021	TTGTTGTCGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTCTGCTGCCATCTTTCTTC	1080
QY	1087	TCTAAATTTGACTCGGAACACATTCGTAACCTCTCCTCCGCCCTTCGTTCCACCCCTCAAG	1148
DB	1081	TCTAAATTTGACTCGGAACACATTCGTAACCTCTCCTCCGCCCTTCGTTCCACCCCTCAAG	1140
QY	1147	TCCGACGATGACACCTCCAAATTTTGTGATGAACACAGAGAAGAAATTCGTGGGTTTCATCTCT	1206
DB	1141	TCTGACGATGACACCTCCAAATTTTGTGATGAACACAGAGAAGAAATTCGTGGGTTTCATCTCT	1200
QY	1207	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCCGTTTGTCGGGTTTTTCG	1266
DB	1201	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCCGTTTGTCGGGTTTTTCG	1260
QY	1267	TACAGCAAGGACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGCTCGGACTCC	1322
DB	1261	TACAGCAAGGACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGCTCGGACTCC	1322
QY	1327	CCTGCCAAGCTAGCTCCTCATGAAAAAGAAATCTTCATCAAAAAGCAAGAGCTCAAGAC	1388
DB	1321	CCTGCCAAGCTAGCTCCTCATGAAAAAGAAATCTTCATCAAAAAGCAAGAGCTCAAGAC	1388
QY	1387	TCTCAGACAAAGTCTCAAGAGTATTTATTTCCGACGCGGCCCTCTTCCTTGCTCCAGG	1446
DB	1381	TCTCAGACAAAGTCTCAAGAGTATTTATTTCCGACGCGGCCCTCTTCCTTGCTCCAGG	1440
QY	1447	ATCTCCCGTCGTTATATGCAAGGATCCGCGCGGGCGCGCTGCTGGCTCTGAGCCGCC	1508
DB	1441	ATCTCCCGTCGTTATATGCAAGGATCCGCGCGGGCGCGCTGCTGGCTCTGAGCCGCC	1500
QY	1507	TGATCCGTA 1515	
DB	1501	TGATCCGTA 1509	
RESULT 6			
ID	ABZ68725	standard; DNA; 1485 BP.	
XX	AC	ABZ68725;	
XX	DT	16-MAY-2003 (first entry)	
XX	DE	Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.	
XX	KW	Human; citron rho/rac-interacting kinase-short kinase; obesity;	
XX	KW	chronic obstructive pulmonary disease; hypertension; diabetes;	
XX	KW	coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;	
XX	KW	gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;	
XX	KW	polycystic ovarian syndrome; fertility; depression; gene; ss.	
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDs	1..1485	
FT		/*tag= a	
FT		/partial	
FT		/product= "citron rho/rac-interacting kinase-short	
FT		kinase"	
XX	PN	WO2003004629-A2.	
XX	PD	16-JAN-2003.	
XX	PF	01-JUL-2002; 2002WO-EP007229.	
XX	PR	02-JUL-2001; 2001US-0301853P.	
XX	PR	10-DEC-2001; 2001US-0337130P.	
XX	PR	25-APR-2002; 2002US-0375015P.	





KW acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;  
 KW asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;  
 KW development; hepatitis; cardiovascular; hypertension; drug screening;  
 KW myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;  
 KW fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;  
 KW hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hiv;  
 KW neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;  
 KW hyperlipidaemia; enzyme; gens; ss.  
 XX Homo sapiens.  
 XX  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 55..6219  
 FT /\*tag= a  
 FT /product= "Human kinase (PKIN)-21"  
 XX  
 PN WO200233099-A2.  
 PD 25-APR-2002.  
 XX  
 PF 20-OCT-2001; 2001WO-US047728.  
 XX  
 PR 20-OCT-2000; 2000US-0242410P.  
 PR 27-OCT-2000; 2000US-0244058P.  
 PR 03-NOV-2000; 2000US-0245708P.  
 PR 09-NOV-2000; 2000US-0247672P.  
 PR 16-NOV-2000; 2000US-0249565P.  
 PR 22-NOV-2000; 2000US-0252730P.  
 PR 01-DEC-2000; 2000US-0250807P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 PI Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;  
 PI Yao MG, Runkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;  
 PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;  
 PI Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;  
 PI Thangavelu K, Khan FA, Ison CH;  
 XX  
 XX WPI; 2002-454603/48.  
 DR P-PSDB; AAE24150.  
 XX  
 XX New human kinase polypeptide, for diagnosing, preventing and treating  
 PT cancer, immune system disorders, growth and development disorders,  
 PT cardiovascular disorders and lipid disorders.  
 XX  
 PS Claim 5; Page 207-209; 210pp; English.  
 XX  
 CC The invention relates human kinases (PKIN) and their corresponding  
 CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing,  
 CC treating and preventing cancer, an immune system disorder (e.g., acquired  
 CC immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,  
 CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting  
 CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),  
 CC cardiovascular disorder (e.g., hypertension, myocardial infarction,  
 CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,  
 CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,  
 CC hyperlipidaemia, obesity), and for assessing the effects of exogenous  
 CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a  
 CC condition or a disease associated with the expression of PKIN in a  
 CC biological sample. A composition comprising PKIN or an agonist or  
 CC antagonist of PKIN is useful for treating a disease or condition  
 CC associated with decreased or increased expression of functional PKIN.  
 CC PKIN is useful in a number of drug screening techniques and to analyse  
 CC the proteome of a tissue or cell type. PKIN DNA is useful for creating  
 CC knockin humanised animals or transgenic animals to model human diseases,  
 CC and in somatic or germline gene therapy. The present sequence is human  
 CC PKIN cDNA  
 XX  
 SQ Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;  
 Query Match 92.7%; Score 1404.2; DB 6; Length 6298;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 60  
 DB 49 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 108  
 QY 61 CCATTGTCACACCGGCTCCAGGCTGAATCTGTTTTCAGGGGAAACACACCTTTATG 120  
 DB 109 CCATTGTCACACCGGCTCCAGGCTGAATCTGTTTTCAGGGGAAACACACCTTTATG 168  
 QY 121 ACTCAACAGCAGATGTCCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
 DB 169 ACTCAACAGCAGATGTCCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 228  
 QY 181 TTTGAAGAAATGCAGTCAGCTCAGCTCTCTGATGAAGATTAAGACGTCAGCAACTTTGTCGG 240  
 DB 229 TTTGAAGAAATGCAGTCAGCTCAGCTCTCTGATGAAGATTAAGACGTCAGCAACTTTGTCGG 288  
 QY 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGGAAAGGACTTCGAA 300  
 DB 289 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGGAAAGGACTTCGAA 348  
 QY 301 GTCAGAAGTCTTGTAGGTTGTGGTCACCTTCTGAAAGTCAGGTGGTAAGAGAGAAAGCA 360  
 DB 349 GTCAGAAGTCTTGTAGGTTGTGGTCACCTTCTGAAAGTCAGGTGGTAAGAGAGAAAGCA 408  
 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTGGCCCGAGAGCAG 420  
 DB 409 ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTGGCCCGAGAGCAG 468  
 QY 421 GTTTCATTTTGGAGGAGCGGAACATATTCTCGAAGCACAAGCCGCTGATCCCC 480  
 DB 469 GTTTCATTTTGGAGGAGCGGAACATATTCTCGAAGCACAAGCCGCTGATCCCC 528  
 QY 481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCT 540  
 DB 529 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCT 588  
 QY 541 GGAGGGGACTTGTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAAACCTGATA 600  
 DB 589 GGAGGGGACTTGTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAAACCTGATA 648  
 QY 601 CAGTTTTACCTAGCTAGCTGAGCTGATTTTGGCTGCTTTCACAGCGTTTCATCTGATGGGATACGTG 660  
 DB 649 CAGTTTTACCTAGCTAGCTGAGCTGATTTTGGCTGCTTTCACAGCGTTTCATCTGATGGGATACGTG 708  
 QY 661 CATCAGACATCAAGCTGAGAACATTTCTGTCACCGCACAGGACACATCAAGTGGTG 720  
 DB 709 CATCAGACATCAAGCTGAGAACATTTCTGTCACCGCACAGGACACATCAAGTGGTG 768  
 QY 721 GATTTTGGATCTCGCGGAAAATGAATTCAAAAGATGGTGAATGCCAAACTCCCGATT 780  
 DB 769 GATTTTGGATCTCGCGGAAAATGAATTCAAAAGATGGTGAATGCCAAACTCCCGATT 828  
 QY 781 GGGACCCAGATTAATGGCTCTGAAAGTGTGATGTGATGAACGGGGATGGAAGGC 840  
 DB 829 GGGACCCAGATTAATGGCTCTGAAAGTGTGATGTGATGAACGGGGATGGAAGGC 888  
 QY 841 ACCTACGGCTGGAGCTGAGCTGGTGGTCACTGGCGTGAATGCTATGAGATGATTTAT 900  
 DB 889 ACCTACGGCTGGAGCTGAGCTGGTGGTCACTGGCGTGAATGCTATGAGATGATTTAT 948  
 QY 901 GGGAGATCCCTCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTC 960  
 DB 949 GGGAGATCCCTCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTC 1008  
 QY 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGACAGTACTTCTTGTATCTGAT 1020  
 DB 1009 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGACAGTACTTCTTGTATCTGAT 1068  
 QY 1021 CAAGCTTGTGTCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCT 1080  
 DB 1069 CAAGCTTGTGTCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCT 1128

QY 1081 TTCTTCTTAAATGACTGGACCAATTCGTAACCTCTCTCCCTCCCTTCTGTTCCCAACC 1140  
 DB 1129 TTCTTCTTAAATGACTGGACCAATTCGTAACCTCTCTCCCTCCCTTCTGTTCCCAACC 1188  
 QY 1141 CTCAAGTCGACGATGACCTCCCAATTTTGTATGACGACGAGAGAAATTCGTTGGTTTCA 1200  
 DB 1189 CTCAAGTCGACGATGACCTCCCAATTTTGTATGACGACGAGAGAAATTCGTTGGTTTCA 1248  
 QY 1201 TCCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGG 1260  
 DB 1249 TCCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGG 1308  
 QY 1261 TTTTCTGATAGCAAGCACTGGGATCTTGTGATGATCTGTTGTGTCGGGTCTG 1320  
 DB 1309 TTTTCTGATAGCAAGCACTGGGATCTTGTGATGATCTGTTGTGTCGGGTCTG 1368  
 QY 1321 GACTCCCTGCGCAAGACTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 DB 1369 GACTCCCTGCGCAAGACTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1428  
 QY 1381 CAAGACTCTCAGCAAGAGTGTCAAGGT 1409  
 DB 1429 CAAGACTCTCAGCAAGAGTGTCAAGAT 1457

RESULT 8

ADAO5643  
 ID ADAO5643 standard; cDNA; 1870 BP.  
 AC  
 AC ADAO5643;  
 XX  
 XX 06-NOV-2003 (first entry)  
 XX  
 XX Human NOV1b encoding cDNA SEQ ID NO:3.  
 DE  
 DE human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
 KW immunomodulator; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; antilipemic; gene therapy; human disease;  
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 2..1870  
 FT /\*tag= a  
 FT /product= "NOV1b"

W02003029424-A2.

PD 10-APR-2003.  
 XX  
 XX 02-OCT-2002; 2002WO-US031373.  
 XX  
 XX 02-OCT-2001; 2001US-0326483P.  
 XX 05-OCT-2001; 2001US-0327435P.  
 XX 05-OCT-2001; 2001US-0327449P.  
 XX 09-OCT-2001; 2001US-0327917P.  
 XX 09-OCT-2001; 2001US-0328029P.  
 XX 09-OCT-2001; 2001US-0328044P.  
 XX 09-OCT-2001; 2001US-0328056P.  
 XX 12-OCT-2001; 2001US-0328849P.  
 XX 15-OCT-2001; 2001US-0329414P.  
 XX 17-OCT-2001; 2001US-0330142P.  
 XX 18-OCT-2001; 2001US-0330309P.  
 XX 22-OCT-2001; 2001US-0341058P.  
 XX 24-OCT-2001; 2001US-0332866P.  
 XX 24-OCT-2001; 2001US-0343629P.  
 XX 29-OCT-2001; 2001US-0349575P.  
 XX 01-NOV-2001; 2001US-0346357P.  
 XX 17-APR-2002; 2002US-0373260P.  
 XX 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.  
 PR 19-APR-2002; 2002US-0373826P.  
 PR 19-APR-2002; 2002US-0373894P.  
 PR 22-APR-2002; 2002US-0374977P.  
 PR 16-MAY-2002; 2002US-0381037P.  
 PR 16-MAY-2002; 2002US-0381038P.  
 PR 16-MAY-2002; 2002US-0381042P.  
 PR 17-MAY-2002; 2002US-0381642P.  
 PR 28-MAY-2002; 2002US-0383656P.  
 PR 29-MAY-2002; 2002US-0383831P.  
 PR 25-JUN-2002; 2002US-0391335P.  
 PR 01-OCT-2002; 2002US-00262511.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;  
 PI Ort T, Gorman L, Zerkhusen BD, Anderson DW, Zhong M, Gatterton E;  
 PI Ji W, Miller CE, Rastelli L, Store DJ, Pena CEA, Shenoy SG;  
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;  
 XX WPI; 2003-381626/36.  
 DR P-PSDB; ADA05644.  
 XX  
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,  
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,  
 PT cancer or dyslipidaemia, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 XX Claim 20; Page 100; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence encodes a human NOVX protein from the present invention.

Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 8; Length 1870;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;





other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention

Query Match 92.3%; Score 1398.2; DB 6; Length 5877;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY	7	ATGTTGAAGTTCAAAATATGGAGCGCGAAATCCCTTTGATGCTGCTGGTCTGCTGCTGAAACCCATT	66
Db	1	ATGTTGAAGTTCAAAATATGGAGCGCGCGAAATCCCTTTGATGCTGCTGGTCTGCTGCTGAAACCCATT	60
QY	67	GCCAACCCGGGCTCCAGGCTGAATCTGTCTTCAGGGGAAACCAACCTTTATGACTCAA	126
Db	61	GCCAGCCGGGCTCCAGGCTGAATCTGTCTTCAGGGGAAACCAACCTTTATGACTCAA	120
QY	127	CAGCAGATGCTCCTCTTCCTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA	186
Db	121	CAGCAGATGCTCCTCTTCCTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA	180
QY	187	GAATGCAGTCAGCCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTCTCCGGGAAGTAT	246
Db	181	GAATGCAGTCAGCCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTCTCCGGGAAGTAT	240
QY	247	TCCGACACCATAGCTGAGTTACAGAGAGCTCAGGCTTCGGCAAGAGCACTTCAAGTCTAGA	306
Db	241	TCCGACACCATAGCTGAGTTACAGAGAGCTCAGGCTTCGGCAAGAGCACTTCAAGTCTAGA	300
QY	307	AGTCTTGTAGTTGTGTGTCATTTTGCTGAAGTGCAGTGTGAAGAGAGAAACCAACCCGG	366
Db	301	AGTCTTGTAGTTGTGTGTCATTTTGCTGAAGTGCAGTGTGAAGAGAGAAACCAACCCGG	360
QY	367	GACATCTATGCTATGAAGTGAAGAGAGAGAGGCTTTATTGGCCACAGAGCAGGTTTCA	426
Db	361	GACATCTATGCTATGAAGTGAAGAGAGAGAGGCTTTATTGGCCACAGAGCAGGTTTCA	420
QY	427	TTTTTTTGAAGAGAGCGGAAACATATTATCTCGAAGCACAAAGCCGTGGATCCCCCAATTA	486
Db	421	TTTTTTTGAAGAGAGCGGAAACATATTATCTCGAAGCACAAAGCCGTGGATCCCCCAATTA	480
QY	487	CAGATAGCCTTTCAAGACAAAATCAGCTTTATCTGGTCATGAATATCAGGCTCGAGGG	546
Db	481	CAGTATGCTTTTCAGGACAAAATCAGCTTTATCTGGTCATGAATATCAGGCTCGAGGG	540
QY	547	GACTTGCCTGTCACTTTTGAATAGATATGAGGACAGTATAGATGAAACCTGATACAGTTT	606
Db	541	GACTTGTCTGCATTTTGAATAGATATGAGGACAGTATAGATGAAACCTGATACAGTTT	600
QY	607	TACCTAGCTAGCTGATTTTGGCTGTTACAGCGTTTCATCTGATGGGATACGTGATCGA	666
Db	601	TACCTAGCTAGCTGATTTTGGCTGTTACAGCGTTTCATCTGATGGGATACGTGATCGA	660
QY	667	GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGATTTT	726
Db	661	GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGATTTT	720
QY	727	GGATCTCCGCGAANAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTGGGACC	786
Db	721	GGATCTCCGCGAANAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTGGGACC	780
QY	787	CCAGATTACATGGCTCCTCGAAGTGTGACTGTGATGAACGGGGATGAAAAGGCACCTAC	846
Db	781	CCAGATTACATGGCTCCTCGAAGTGTGACTGTGATGAACGGGGATGAAAAGGCACCTAC	840
QY	847	GGCTTGAGCTGTGACTGGTGGTCAGTGGGGCTGATTTGCCCTATCAGATGATTTATGGGAGA	906
Db	841	GGCTTGAGCTGTGACTGGTGGTCAGTGGGGCTGATTTGCCCTATCAGATGATTTATGGGAGA	900
QY	907	TCCCCCTTCGACAGAGGAAACCTCTGCCAGAACCTTCAATAACATTTAGAAATTCACGCGG	966

PT polynucleotide, useful in preventing, ameliorating or treating diseases  
PT associated with human CR1K dysfunction, e.g. obesity, diabetes or  
PT Alzheimer's disease.

XX Disclosure; Page 217-222; 237pp; English.

XX The invention relates to an isolated polynucleotide encoding a human  
CC citron rho/rac-interacting kinase polypeptide. The isolated  
CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the  
CC specification. The human citron rho/rac-interacting kinase (CR1K)  
CC polypeptide and polynucleotide are useful in preventing, ameliorating, or  
CC treating diseases associated with human CR1K dysfunction such as obesity  
CC and obesity-associated comorbidities (e.g. hypertension, coronary artery  
CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of  
CC cancer including endometrial, breast, prostate and colon cancer),  
CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood  
CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's  
CC disease), chronic obstructive pulmonary disease, or diabetes. These can  
CC also be used to treat pain associated with the disorders. The human CR1K  
CC polypeptide is also useful in diagnostic assays or in genetic testing.  
CC The expression vector or the reagent is useful in preparing a medicament  
CC for modulating the activity of a human CR1K in a disease, e.g. obesity, a  
CC central nervous system disorder, or chronic obstructive pulmonary  
CC disease. The fusion protein is useful for generating antibodies against a  
CC CR1K polypeptide and for use in various assay systems. The methods are  
CC useful in producing and detecting the polynucleotide and polypeptide and  
CC in screening for agents that modulate the activity of the human CR1K  
CC polypeptide. This polynucleotide sequence represents a DNA sequence  
CC relating to the human CR1K protein of the invention

XX SQ Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 9; Length 6156;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTTGGATGCTGGTCTGTAACCCATT 56  
DB 1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTTGGATGCTGGTCTGTAACCCATT 60  
QY 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAACACCCCTTTATGACTCAA 126  
DB 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAACACCCCTTTATGACTCAA 120  
QY 127 CAGCAGATGCTCCTCTTCCGAGAAAGGATATAGATGCGCTCTTTCTCTTTGAA 186  
DB 121 CAGCAGATGCTCCTCTTCCGAGAAAGGATATAGATGCGCTCTTTCTCTTTGAA 180  
QY 187 GAATGCAGTCAGCTCTCTGATGAAGATTAGCAGCTGAGCAACTTTGTCGGAAGTAT 246  
DB 181 GAATGCAGTCAGCTCTCTGATGAAGATTAGCAGCTGAGCAACTTTGTCGGAAGTAT 240  
QY 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAATCAGA 306  
DB 241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAATCAGA 300  
QY 307 AGTCTTGATGTTGGTTCACCTTCTGAGTGCAGTGGTGAAGAGAAACCCGG 366  
DB 301 AGTCTTGATGTTGGTTCACCTTCTGAGTGCAGTGGTGAAGAGAAACCCGG 360  
QY 367 GACATCTATGCTATGAAGTGTGAAGAAAGAGCTTTTATGGCCAGGAGAGGTTTCA 426  
DB 361 GACATCTATGCTATGAAGTGTGAAGAAAGAGCTTTTATGGCCAGGAGAGGTTTCA 420  
QY 427 TTTTGTGAGGAAGCGGAACATATTATCTGAGGACACAGCCCGTGGATCCCCCAATTA 486  
DB 421 TTTTGTGAGGAAGCGGAACATATTATCTGAGGACACAGCCCGTGGATCCCCCAATTA 480  
QY 487 CAGTATGCTCTTTCAGGACAAAATACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 546  
DB 481 CAGTATGCTCTTTCAGGACAAAATACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 540  
QY 547 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTAGATGAAAAACCTGATACAGTTT 606

DB 541 GACTTGTCTCACTTTTGAATAGATATGAGACCAAGTTAGATGAAAAACCTGATACAGTTT 600  
QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGCTTCACTGATGGGATACGTGATCGA 666  
DB 601 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGCTTCACTGATGGGATACGTGATCGA 660  
QY 667 GACATCAAGCTGAGACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726  
DB 661 GACATCAAGCTGAGACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720  
QY 727 GGATCTGCGCGAAAAATGAATTTCAAAACAGATGCTGAATGCCAAACTCCCGATTTGGAGC 786  
DB 721 GGATCTGCGCGAAAAATGAATTTCAAAACAGATGCTGAATGCCAAACTCCCGATTTGGAGC 780  
QY 787 CCAGATTACATGCTCTGAGTCTGACTGCTGATGAAACCGGATGGAAGGACACCTAC 846  
DB 781 CCAGATTACATGCTCTGAGTCTGACTGCTGATGAAACCGGATGGAAGGACACCTAC 840  
QY 847 GGCCTGGAATCTGACTGCTGAGTGGGCTGATTCGCTATGAGATGATTTATGGGAGA 906  
DB 841 GGCCTGGAATCTGACTGCTGAGTGGGCTGATTCGCTATGAGATGATTTATGGGAGA 900  
QY 907 TCCGCTTCGAGAGGAAACCTCTGCCAGAACCTTCAATTAACATTAATTTCCAGCGG 966  
DB 901 TCCGCTTCGAGAGGAAACCTCTGCCAGAACCTTCAATTAACATTAATTTCCAGCGG 960  
QY 967 TTTTGAATTTCCAGATGACCCCAAAAGTGAGCTGACTTTCTTTGATCTGATTTCAAGC 1026  
DB 961 TTTTGAATTTCCAGATGACCCCAAAAGTGAGCTGACTTTCTTTGATCTGATTTCAAGC 1020  
QY 1027 TTGTTGTGCGGCCAGAGAGAGACTGAAATTTGAAGGCTTTTGTCTGCCATTCCTTCTTC 1086  
DB 1021 TTGTTGTGCGGCCAGAGAGAGACTGAAATTTGAAGGCTTTTGTCTGCCATTCCTTCTTC 1080  
QY 1087 TCTAAATTTGACTGGAACACATTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAG 1146  
DB 1081 TCTAAATTTGACTGGAACACATTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAG 1140  
QY 1147 TCCGACCATGACACTCCAAATTTTGAATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1206  
DB 1141 TCTGACGATGACACTCCAAATTTTGAATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1200  
QY 1207 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGGGGTTTTCG 1266  
DB 1201 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGGGGTTTTCG 1260  
QY 1267 TACAGCAAGGCACTGGGATTTCTTGTGATAGTCTGAGTCTGTTGTGCGGTTCTGACTCC 1326  
DB 1261 TACAGCAAGGCACTGGGATTTCTTGTGATAGTCTGAGTCTGTTGTGCGGTTCTGACTCC 1320  
QY 1327 CCGTCCAGCTGAGCTCAGTGAAGAAAGAAATTTCTCATTAAGCAAGAGCTTCAAGAC 1386  
DB 1321 CCGTCCAGCTGAGCTCAGTGAAGAAAGAAATTTCTCATTAAGCAAGAGCTTCAAGAC 1380  
QY 1387 TCTCAGGACAGTGTCAAGGT 1409  
DB 1381 TCTCAGGACAGTGTCAAGAT 1403

RESULT 11

ABQ78870

ID ABQ78870 standard; cdna; 6165 BP.

XX ABQ78870;

XX 10-OCT-2002 (first entry)

XX Human kinase cdna #1.

XX Human; kinase; enzyme; serine-threonine kinase; neotrophic; cytostatic;

XX Citron rho-interacting kinase; gene therapy; mental disorder; cancer;  
XX gene; ss.

XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
XX	PH	1. .6165
FT	CDS	/tag= a
FT		/product= "Kinase"
FT	variation	replace(5218,G)
FT		/tag= b
FT	variation	/standard_name= "Single nucleotide polymorphism"
FT		replace(6065,G)
FT		/tag= b
FT		/standard_name= "Single nucleotide polymorphism"
XX	XX	W0200259325-A2.
XX	PD	01-AUG-2002.
XX	PB	20-DEC-2001; 2001WO-US050497.
XX	PR	27-DEC-2000; 2000US-0258335P.
XX	PA	(LEXI-) LEXICON GENETICS INC.
XX	PI	Yu X, Miranda M, Friiddle CJ;
XX	WP	WPI; 2002-599796/64.
DR	P-PSDB	ABB81927.
XX	XX	
PT	Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in gene therapy of disorders and diseases e.g. cancer and pharmacogenomic applications.	
XX	Claim 1; Page 37-39; 50pp; English.	
CC	The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nontropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention	
XX	Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;	
Query Match	92.3%; Score 1398.2; DB 6; Length 6165;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1400; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
QY	7 ATGTTGAAGTTCAAATATGAGCGGGAACTCCTTTGGATGCTGTGCTGACCAACCATT	66
Db	1 ATGTTGAAGTTCAAATATGAGCGGGAACTCCTTTGGATGCTGTGCTGACCAACCATT	60
QY	67 GCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCAA	126
Db	61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCAA	120
QY	127 CAGCAGATCTCTCTTCCAGAGAGGATATTAGTGCCCTTTGTTCTTTTGA	186
Db	121 CAGCAGATCTCTCTTCCAGAGAGGATATTAGTGCCCTTTGTTCTTTTGA	180
QY	187 GAATGCAGTCAGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCGGGAAGTAT	246
Db	181 GAATGCAGTCAGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCGGGAAGTAT	240
QY	247 TC CGACACCATAGCTAGTTACAGAGCTCCAGGCCCTCGGCAAAAGGACTTCGAAAGTCAGA	306
Db	241 TC CGACACCATAGCTAGTTACAGAGCTCCAGGCCCTCGGCAAAAGGACTTCGAAAGTCAGA	300

DB 1381 TCTCAGGACCAAGTGTCACAGAT 1403

RESULT 12

AAL55214

ID AAL55214 standard; DNA; 6165 BP.

AC AAL55214;

XX 01-MAY-2003 (first entry)

XX Human CRK encoding DNA sequence, SEQ ID No 1.

XX Anorectic; hypotensive; cardiac; antilipemic; cerebroprotective;

XX antitumor; osteopathic; antiarthritic; cytostatic; antidepressant;

XX immunomodulator; antineoplastic; tranquilizer; antiparkinsonian; neurotropic;

XX neuroprotective; antiinflammatory; antidiabetic; analgesic;

XX human citron rho/rac-interacting kinase; enzyme; CRK; ameliorating;

XX obesity; comorbidities; cancer; anorexia; cachexia; bulimia;

XX central nervous system disorder; chronic obstructive pulmonary disease;

XX diabetes; pain; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..6165

XX /\*tag= a

XX /product= "Human CRK protein"

XX WO2003004523-A1.

XX 16-JAN-2003.

XX 28-JUN-2002; 2002WO-EP007156.

XX 02-JUL-2001; 2001US-0301841P.

XX 11-DEC-2001; 2001US-0338651P.

XX 25-APR-2002; 2002US-0375014P.

XX (FARB ) BAYER AG.

XX Zhu Z;

XX WPI; 2003-221576/21.

XX P-PSDB; AAO26959.

XX New human citron rho/rac-interacting kinase (CRK) polypeptide and

XX polynucleotide, useful in preventing, ameliorating or treating diseases

XX associated with human CRK dysfunction, e.g. obesity, diabetes or

XX Alzheimer's disease.

XX Example 1; Fig 1; 237pp; English.

XX The invention relates to an isolated polynucleotide encoding a human

XX citron rho/rac-interacting kinase polypeptide. The isolated

XX polynucleotide comprises a 6165 or 8603 base pair sequence, given in the

XX specification. The human citron rho/rac-interacting kinase (CRK)

XX polypeptide and polynucleotide are useful in preventing, ameliorating, or

XX treating diseases associated with human CRK dysfunction such as obesity

XX and obesity-associated comorbidities (e.g. hypertension, coronary artery

XX disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of

XX cancer including endometrial, breast, prostate and colon cancer),

XX anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood

XX disorders, anxiety disorders, Parkinson's disease or Alzheimer's

XX disease), chronic obstructive pulmonary disease, or diabetes. These can

XX also be used to treat pain associated with the disorders. The human CRK

XX polypeptide is also useful in diagnostic assays or in genetic testing.

XX The expression vector or the reagent is useful in preparing a medicament

XX for modulating the activity of a human CRK in a disease, e.g. obesity, a

XX central nervous system disorder, or chronic obstructive pulmonary

XX disease. The fusion protein is useful for generating antibodies against a

XX CRK polypeptide and for use in various assay systems. The methods are

CC useful in producing and detecting the polynucleotide and polypeptide and

CC in screening for agents that modulate the activity of the human CRK

CC polypeptide. This polynucleotide sequence represents a DNA sequence

CC encoding a human CRK protein of the invention

XX

XX Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

XX

XX Query Match 92.3%; Score 1398.2; DB 9; Length 6165;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTGGATGCTGGTGTGCTGAACCCATT 66

DB 1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTGGATGCTGGTGTGCTGAACCCATT 60

QY 67 GCCAACCCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCCCTTATGACTCAA 126

DB 61 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCCCTTATGACTCAA 120

QY 127 CAGCAGATGTTCTCTCTTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186

DB 121 CAGCAGATGTTCTCTCTTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

QY 187 GAATGACGTACGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGAAGTAT 246

DB 181 GAATGACGTACGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGAAGTAT 240

QY 247 TCCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTACA 306

DB 241 TCCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTACA 300

QY 307 AGCTTTGAGTGTGTGTCACCTTTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 366

DB 301 AGCTTTGAGTGTGTGTCACCTTTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 360

QY 367 GACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 426

DB 361 GACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420

QY 427 TTTTGTGAGGAGAGCGGAACATATTCTCGAAGCACAAGCCGCTGGATCCCCCAATTA 486

DB 421 TTTTGTGAGGAGAGCGGAACATATTCTCGAAGCACAAGCCGCTGGATCCCCCAATTA 480

QY 487 CAGTATGCTTTTCAGGACAAAATCAGCTTTATCTGCTCATGATATACAGCTGGAGGG 546

DB 481 CAGTATGCTTTTCAGGACAAAATCAGCTTTATCTGCTCATGATATACAGCTGGAGGG 540

QY 547 GACTTGTCTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGATAAACCCTGATACAGTTT 606

DB 541 GACTTGTCTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGATAAACCCTGATACAGTTT 600

QY 607 TACCTAGCTGAGCTGATTTGGCTGTTTCACAGCGTTTATCTGATGGGATACGTCATCGA 666

DB 601 TACCTAGCTGAGCTGATTTGGCTGTTTCACAGCGTTTATCTGATGGGATACGTCATCGA 660

QY 667 GACATCAAGCTCTGAGAACATTTCTGTTGACCGCACGACACATCAAGCTGGTGGATTTT 726

DB 661 GACATCAAGCTCTGAGAACATTTCTGTTGACCGCACGACACATCAAGCTGGTGGATTTT 720

QY 727 GGATCTCGCGGAAATGAATTTCAACAAGATGGTGAATGCCAACTCCGATTTGGGACC 786

DB 721 GGATCTCGCGGAAATGAATTTCAACAAGATGGTGAATGCCAACTCCGATTTGGGACC 780

QY 787 CCAGATTACATGGCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 846

DB 781 CCAGATTACATGGCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 840

QY 847 GGCCTGAGCTGTGACTGGTGTGCTGAGTGGGCTGATTCCTCTATGAGATGATTTATGGGAGA 906

DB 841 GGCCTGAGCTGTGACTGGTGTGCTGAGTGGGCTGATTCCTCTATGAGATGATTTATGGGAGA 900

QY 907 TCCCTCTCGCAGAGGAACTCTGCCAGAACCTTCAATTAACATTATGATTTTCCAGCGG 966

Dd	901	TCCCCCTTCGAGGGGAACCTCTGCAGAACCTTCAATAAATATTGAATTTCCAGCGG	960
Qy	967	TTTTTGAAATTTCCAGATGACCCCAAAGTCAGCAGTGACTTTTCTTGATCTGTATCCAAGC	1026
Dd	961	TTTTTGAAATTTCCAGATGACCCCAAAGTCAGCAGTGACTTTTCTTGATCTGTATCCAAGC	1020
Qy	1027	TTGTTGTGGCGGCAGAAAAGAGAGACTGAAGTTTGAAGGTCCTTGCTGCCATCCTTTCTTC	1086
Dd	1021	TTGTTGTGGCGGCAGAAAAGAGAGACTGAAGTTTGAAGGTCCTTGCTGCCATCCTTTCTTC	1080
Qy	1087	TCTAAAAATTCGACTGGAAACAACATTCGTAATCTCTCTCCCCCTTCGTTGCCACCCTCAAG	1146
Dd	1081	TCTAAAAATTCGACTGGAAACAACATTCGTAATCTCTCTCCCCCTTCGTTGCCACCCTCAAG	1140
Qy	1147	TCCGACGATGACACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGGTTTCACTCT	1206
Dd	1141	TCTGACGATGACACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGGTTTCACTCT	1200
Qy	1207	CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTGTGGGGTTTTCG	1266
Dd	1201	CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTGTGGGGTTTTCG	1260
Qy	1267	TACAGCAAGGCACCTGGGGATTCCTGGTAGATCTGAGTCTGTTGTGCGGTCCTGGACTCC	1326
Dd	1261	TACAGCAAGGCACCTGGGGATTCCTGGTAGATCTGAGTCTGTTGTGCGGTCCTGGACTCC	1320
Qy	1327	CCTGCCAAGACTAGCTCCATGGAAAAGAACTTCTCATCAAAAAGCAAGAGCTACAAGAC	1386
Dd	1321	CCTGCCAAGACTAGCTCCATGGAAAAGAACTTCTCATCAAAAAGCAAGAGCTACAAGAC	1380
Qy	1387	TCTCAGCACAGTGTCAAGGT	1409
Dd	1381	TCTCAGCACAGTGTCAAGAT	1403

RESULT 13

RESOL1 13  
AAL55215  
ID AAL55215 standard; DNA: 8603 BP.

XX  
AC AAL55215;

XX DT 01-MAY-2003 (first entry)

XX DE Human CR1K related DNA sequence. SEQ ID No 4.

xx  
KW Anorectic; hypotensive; cardiac; antilipaemic; cerebroprotective;  
KW antitoxic; osteopathic; antichratic; cytostatic; antidepressant;  
KW immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;  
KW neuroprotective; antiinflammatory; antidiabetic; analgesic;  
KW human catron rho/rac-interacting kinase; enzyme; CRK; ameliorating;  
KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;  
KW central nervous system disorder; chronic obstructive pulmonary disease  
KW diabetes; pain; ds.

XX Homo sapiens. OS

XX PN WO2003004523-A1.

XX  
PD  
16-JAN-2003.

XX PF 28-JUN-2002:

XX  
PR 02-JUL-2001: 2001US-0301841P.

PR 11-DEC-2001; 2001US-0338651P.  
PR 25-APR-2002; 2002US-0375014P.

XX  
DA (FARR) RAYVER AG

XX  
DT  
760 2.

XX

XX

polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CR1K dysfunction, e.g. obesity, diabetes or Alzheimer's disease.

XX  
PS Disclosure: Fig 4: 237pp; English.

The invention relates to an isolated polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer), anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polynucleotide sequence represents a DNA sequence relating to the human CRIK protein of the invention

Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other; XX SO

Query Match	92.3%	Score 1398.2	DB 9	Length 8603
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1400	Conservative	0	Mismatches	3
			Indels	0
			Caps	0

Qy	7	ATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGGTCTGCTGAACCCATT	66
Db	1	ATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGGTCTGCTGAACCCATT	60
Qy	67	GCCAAACGGGCGCTCCAGGCTGAATCTGTCTTCCAGGGGAACACCCCTTTATGACTCAA	126
Db	61	GCCAGCGGGCCTCAGGCTGAATCTGTCTTCCAGGGGAACACCCCTTTATGACTCAA	120
Qy	127	CAGCAGATGTCCTCTTTTCCGAGAAGGGAATTATGATGCGCCTCTTTGTTCTCTTTGAA	186
Db	121	CAGCAGATGTCCTCTTTTCCGAGAAGGGAATTATGATGCGCCTCTTTGTTCTCTTTGAA	180
Qy	187	GAATGCAGTCAGCGCTGCTCTGATGAAGATTAAGCAAGTGAACAACTTTGTCGCGGAAGTAT	246
Db	181	GAATGCAGTCAGCGCTGCTCTGATGAAGATTAAGCAAGTGAACAACTTTGTCGCGGAAGTAT	240
Qy	247	TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGCGAAGACTTCGGAAGTCAGA	306
Db	241	TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGCGAAGACTTCGGAAGTCAGA	300
Qy	307	AGTCTTGTAGGTTGTGTCATCTTTGCTGAAGTCAGGTGCTTAAGAGAGAAAGCAACCGGG	366
Db	301	AGTCTTGTAGGTTGTGTCATCTTTGCTGAAGTCAGGTGCTTAAGAGAGAAAGCAACCGGG	360
Qy	367	GACATCTATGCTATGAAGTGTATGAAGAAAGGCTTTATTGGCCGAGGACAGGTTTCA	426
Db	361	GACATCTATGCTATGAAGTGTATGAAGAAAGGCTTTATTGGCCGAGGACAGGTTTCA	420
Qy	427	TTTTTTTGAGGAAGAGCGGGAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA	486
Db	421	TTTTTTTGAGGAAGAGCGGGAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTA	480
Qy	487	CAGTATGCCCTTTCAGGACAAAATTCACCTTTATCTGGTCATGAAATATCAGCCTGAGGG	546
Db	481	CAGTATGCCCTTTCAGGACAAAATTCACCTTTATCTGGTCATGAAATATCAGCCTGAGGG	540
Qy	547	GACTTGTGTCATCTTTTGAATAGATATGAGGACCAAGTATAGTAAACCTGTATACAGTTT	606



Db 541 GACTTGCTGACCTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGTACACAGTTT 600  
 Qy 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTCATCGA 666  
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RESULT 14

AAD39191  
 ID AAD39191 standard; cDNA; 6574 BP.

XX  
 AC AAD39191;

XX 04-OCT-2002 (first entry)

XX Human MDPK cDNA.

XX Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;  
 KW tumorigenesis; tumor growth; tumor metastasis; viral infection;  
 XW skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;

immune disorder; neoplastic disorder; gene therapy; gene; ss.

Homo sapiens.

Key Location/Qualifiers

5'UTR 1..18

CDS /\*tag= a

19..6180

/\*tag= b

/\*product= "Human MDPK protein"

misc\_feature 19..6177

/\*tag= c

/\*note= "This region is specifically referred in claim 1

as SEQ ID NO:3"

6181..6574

3'UTR /\*tag= d

WO200234896-A2.

02-MAY-2002.

23-OCT-2001; 2001WO-US050636.

23-OCT-2000; 2000US-0242429P.

(MILL-) MILLENNIUM PHARM INC.

Kapeller-Libermann R;

WPI; 2002-479720/51.

P-PSDB; AAE24079.

Human myotonic dystrophy type protein kinase polypeptide and

polynucleotide useful for prognosticating, diagnosing, preventing or

inhibiting tumorigenesis, tumor growth, tumor metastasis and viral

infection.

Claim 1; Fig 1; 148pp; English.

The invention relates to human myotonic dystrophy type protein kinase

(MDPK) polypeptides designated as 13245 and nucleic acid molecules

encoding such polypeptides. 13245 molecules are used to develop

diagnostic and therapeutic agents for prognosticating, diagnosing,

preventing, inhibiting, alleviating or curing MDPK-related disorders.

Polypeptides of the invention are used to develop diagnostic and

therapeutic agents for 13245-mediated or related disorders such as

tumorigenesis, tumor growth, tumour metastasis, viral infection of a

cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),

immune disorders and neoplastic disorders. The invention is also used in

gene therapy. The present sequence is human MDPK cDNA

Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;

Query Match 92.3%; Score 1397.8; DB 6; Length 6574;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGTGAA 60

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Qy 61 CCCATTGCCAACCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 120

Db 73 CCCATTGCCAGCGCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCACCTTTATG 132

Qy 121 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 180

Db 133 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 192

Qy 181 TTTGAAGAATGCAAGTCAAGCTGCTCGATGAAGATTAAAGCACGTCGACACTTTGTCGG 240

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Db  
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RESULT 15  
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XX  
AC ADF60992;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Pain associated human 2207 gene.  
XX  
KW Pain modulation; pain disorder; painful disorder; potassium channel;  
KW kinase expression; inflammatory pain; chronic pain; neuropathic pain;  
KW causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;  
KW analgesic; antiinflammatory; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2003153525-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 19-DEC-2002; 2002US-00325430.  
XX  
PR 19-DEC-2001; 2001US-0341953P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Silos-Santiago I, Rosenfeld JB;  
XX  
DR WPI; 2003-897732/82.  
DR P-PSDB; ADF60994.  
XX  
FT Identifying a compound capable of treating a pain disorder comprises  
FT assaying the ability of the compound to modulate specific, e.g., kinases  
FT or potassium channel, nucleic acid expression or polypeptide activities.  
XX  
PS Disclosure; SEQ ID NO 10; 80pp; English.  
XX  
CC The present invention relates to a method for identifying a compound  
CC capable of modulating pain or painful disorders. The method comprises  
CC assaying the ability of the compound to modulate specific nucleic acid  
CC expression or polypeptide activity e.g. potassium channel, or kinase  
CC expression/activity. The method and compounds are useful for treating  
CC pain or painful disorders e.g. inflammatory pain, chronic pain,  
CC neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache  
CC pain and tissue pain. The present sequence encodes a human protein  
CC associated with pain.  
XX  
SQ Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;  
Query Match 92.3%; Score 1397.8; DB 10; Length 6574;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 60  
Db 13 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 72  
Qy 61 CCCATTCACCGCGGCTCCAGCTGATCTGCTTCCAGGGGAAACACACCTTTATG 120  
Db 73 CCCATTCACCGCGGCTCCAGCTGATCTGCTTCCAGGGGAAACACACCTTTATG 132  
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Db 133 ACTCAACAGCAGATGCTCTCTTTCCGAGAGGAGATATAGATGCCCTCTTTGTTCTC 192





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 02:03:14 ; Search time 6341 Seconds  
(without alignments)  
11298.517 Million cell updates/sec

Title: US-10-724-594-1  
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Sequence: 1 gggagagatgtgaagttaa.....tctgagcgcctgatccgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb\_pl.\*  
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12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1510.2	99.7	2066	6 AX642956	Sequence
4	1505.8	99.4	1785	6 AX671044	Sequence
5	1481.8	97.8	1485	6 AX671037	Sequence
6	1404.2	92.7	6298	6 AX504254	Sequence
7	1404.2	92.7	8576	9 AY257469	Sequence
8	1398.2	92.4	1799	9 AY209000	Homo sapi
9	1398.2	92.3	5877	6 AX574427	Sequence
10	1398.2	92.3	6156	6 AX671112	Sequence
11	1398.2	92.3	6165	6 AX574425	Sequence
12	1398.2	92.3	6165	6 AX671105	Sequence
13	1398.2	92.3	8603	6 AX671108	Sequence
14	1397.8	92.3	6574	6 AX429512	Sequence
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22	1082	71.4	1386	10 AF070065	Rattus no
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## ALIGNMENTS

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LOCUS AR253937 1515 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 1 from patent US 6479269.  
ACCESSION AR253937  
VERSION AR253937.1 GI:27302420  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1515)  
Webster, M., Yan, C., Di Francesco, V. and Beasley, E. M.  
AUTHORS Isolated human kinase proteins, nucleic acid molecules encoding  
TITLE human kinase proteins, and uses thereof  
JOURNAL Patent: US 6479269-A 1 12-NOV-2002;  
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RESULT 2
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LOCUS
DEFINITION
ACCESSION
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VERSION
AR453415.1
KEYWORDS
SOURCE
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    ORGANISM
        Unknown.
    UNCLASSIFIED.
    1 (bases 1 to 1515)
    Webster,M., Yan,C., Di Francesco, V. and Beasley,E.M.
    TITLE
        Isolated human kinase proteins, nucleic acid molecules encoding
        human kinase proteins, and uses thereof
    JOURNAL
        Patent: US 6680188-A 1 20-JAN-2004;
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    source

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RESULT 3

AX642956  
LOCUS AX642956 2066 bp DNA linear PAT 24-FEB-2003  
DEFINITION Sequence 33 from Patent WO01096547.  
ACCESSION AX642956  
VERSION AX642956.1 GI:28550096  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,  
Gandhi,A.R., Tribouley,C.M., Walla,N., Yao,M.G., Lu,D.A.,  
Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,  
Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,  
Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,  
Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,  
Elliot,V.S., Thangavelu,K., Batra,S. and Ison,C.H.  
HUMAN KINASES  
TITLE  
JOURNAL  
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Db 128 ACTCAACAGCAGATGCTCTCTTCCAGAGAGGATATTAGATGCGCTCTTTCTTCTC 187  
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Db 1429 CAAGACTCTCAGCAAGTGTACAGGT 1457

## RESULT 7

AY257469 8576 bp mRNA linear PRI 23-APR-2003  
LOCUS Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete cds.

AY257469  
VERSION AY257469.1 GI:30088969

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (Bases 1 to 8576)

JOURNAL Huang, C.Q., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.

Submitted (18-MAR-2003) Department of Biochemistry and Molecular

Biology, Basic Medicine, Suzhou University, Renming Road 48,

Suzhou, Jiangsu 215007, China

Location/Qualifiers

1. 8576

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="12"

/map="12q24.23"

1. 8576

/gene="CIT"

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54. 6137

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/note="serine/threonine protein kinases"

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/protein\_id="AAPI3528.1"

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Query Match 92.7%; Score 1404.2; DB 9; Length 8576;  
Best Local Similarity 99.8%; Pred. No. 0;  
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QY 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGGACTTCGAA 300  
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LOCUS      5877 bp      DNA      linear      PAT 07-JAN-2003
DEFINITION Sequence 3 from Patent WO02059325.
ACCESSION AX574427
VERSION    AX574427.1 GI:27551752
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Yu, X., Miranda, M. and Friddle, C.J.
TITLE      Human kinases and polynucleotides encoding the same
JOURNAL    Patent: WO 02059325-A 3 01-AUG-2002;
           Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      92.3%; Score 1398.2; DB 6; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 ATGTTGAAGTTCAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTGCTGAACCCATT 66
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RESULT 10  
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LOCUS AX671112 6156 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 8 from Patent WO03004523.  
ACCESSION AX671112  
VERSION AX671112.1 GI:29329572  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Zhu, Z.  
Regulation of human citron rho/rac-interacting kinase  
Patent: WO 03004523-A 8 16-JAN-2003;  
Bayer Aktiengesellschaft (DE)  
Location/Qualifiers  
1. .6156  
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Best Local Similarity 99.8%; Pred. No. 0;  
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Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2440	93.8	2027	Q86UQ9	Q86uq9 homo sapien
2	2425	93.2	482	Q6XUH8	Q6xuh8 homo sapien
3	2425	93.2	482	AAP43922	Aap43922 homo sapi
4	2271.5	87.3	494	Q88937	Q88937 mus musculu
5	2172.5	83.5	2055	Q88938	Q88938 mus musculu
6	2157.5	82.9	448	Q88527	Q88527 rattus norv
7	929	35.7	717	Q8AXM0	Q8axm0 xenopus lae
8	929	35.7	1551	Q6D737	Q6dt37 homo sapien
9	922	35.4	1854	Q9VYF8	Q9vty8 drosophila
10	897.5	34.5	1592	Q01583	Q01583 caenorhabdi
11	896.5	34.5	492	Q86XZ8	Q86xz8 homo sapien
12	896.5	34.5	933	Q86TJ1	Q86tj1 homo sapien
13	896.5	34.5	1711	Q9Y5S2	Q9y5s2 homo sapien
14	896.5	34.5	1760	Q9UJUS	Q9ulus homo sapien
15	891	34.2	496	Q39646	Q39646 homo sapien
16	891	34.2	1573	Q27PW87	Q27pw87 anopheles g
17	891	34.2	1638	Q86XX2	Q86xx2 homo sapien
18	891	34.2	1719	Q86XX3	Q86xx3 homo sapien
19	891	34.2	1732	Q54874	Q54874 rattus norv
20	890	34.2	1638	Q81WQ7	Q81wq7 homo sapien
21	883	33.9	1702	Q54875	Q54875 rattus norv
22	883	33.9	1713	Q27TT49	Q27tt49 rattus norv
23	880	33.9	1713	Q27TT50	Q27tt50 mus musculu
24	876.5	33.7	1173	Q92199	Q92199 caenorhabdi
25	874	33.6	1370	Q273732	Q273732 xenopus lae
26	867	33.3	1375	Q90V37	Q90v37 brachydanio
27	866.5	33.3	1354	Q70335	Q70335 mus musculu
28	865	33.2	1388	1 ROC1_MOUSE	1 ROC1_MOUSE
29	864.5	33.2	1354	1 ROC2_HUMAN	1 ROC2_HUMAN
30	862.5	33.1	1369	1 ROC1_RAT	1 ROC1_RAT
31	860.5	33.1	1354	1 ROC1_RABIT	1 ROC1_RABIT

32	860.5	33.1	1388	1 ROC2_BOVIN	Q28021 bos taurus
33	857.5	33.0	629	2 Q6P5Z6	Q6p5z6 homo sapien
34	857.5	33.0	629	2 AAH62553	AAh62553 homo sapi
35	857.5	33.0	1613	2 Q44368	Q44368 drosophila
36	857.5	33.0	1637	2 Q9W1B0	Q9w1b0 drosophila
37	853.5	32.8	1388	1 ROC2_MOUSE	P70336 mus musculu
38	847	32.6	631	1 DMK_MOUSE	P54265 mus musculu
39	837.5	32.2	1379	1 ROC2_RAT	Q62868 rattus norv
40	822.5	31.6	639	1 DMK_HUMAN	Q09013 homo sapien
41	809	31.1	1390	2 Q9U779	Q9u779 drosophila
42	809	31.1	1390	2 Q9VXE3	Q9vxe3 drosophila
43	809	31.1	1390	2 Q961D4	Q961d4 drosophila
44	778.5	29.9	865	2 Q98SN6	Q98sn6 gallus gall
45	763.5	29.3	289	2 O00565	O00565 homo sapien

## ALIGNMENTS

### RESULT 1

Q86UQ9	PRELIMINARY;	PRT; 2027 AA.
ID	Q86UQ9	
AC	Q86UQ9;	
DT	01-JUN-2003 (Tremblrel. 24, Created)	
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)	
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)	
DE	Rho/rac-interacting citron kinase.	
GN	Name=CIT;	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;	
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.	
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	
DR	HSSP; AY257469; AAPI3528.1; -	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0005524; P:ATP binding; IEA.	
DR	GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.	
DR	GO; GO:0005089; P:small GTPase regulatory/interacting protein. .; IEA.	
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.	
DR	GO; GO:0006469; P:protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR001180; Citron.	
DR	InterPro; IPR005479; Cphb synth_L_D2.	
DR	InterPro; IPR002219; DAG_Es-bind_.	
DR	InterPro; IPR011009; Kinase_like.	
DR	InterPro; IPR001849; PH.	
DR	InterPro; IPR000961; Pkinase C.	
DR	InterPro; IPR000719; prot_kinase.	
DR	InterPro; IPR000861; REM repeat.	
DR	InterPro; IPR002290; Ser_thr_kinase.	
DR	InterPro; IPR008271; Ser_thr_pkin_AS.	
DR	Pfam; PF00130; Cl_1; 1.	
DR	Pfam; PF00780; CNH; 1.	
DR	Pfam; PF00169; PH; 1.	
DR	Pfam; PF00069; Pkinase; 1.	
DR	Pfam; PF00433; Pkinase C; 1.	
DR	ProDom; PD000001; Prot_kinase; 1.	
DR	SMART; SM00109; Cl; 1.	
DR	SMART; SM00036; CNH; 1.	
DR	SMART; SM00233; PH; 1.	
DR	SMART; SM00220; S_TK; 1.	
DR	SMART; SM00133; S_TK_X; 1.	
DR	PROSITE; PS00867; CFSASE 2; UNKNOWN 1.	
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.	
DR	PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.	
DR	PROSITE; PS50003; PH_DOMAIN; 1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 2027 AA; 231429 MW; 681D8C3F661F357B CRC64;

Query Match 93.8%; Score 2440; DB 2; Length 2027;  
Best Local Similarity 99.6%; Pred. No. 2.1e-154;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
QY 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
DB 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240  
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMIIYGR 300  
DB 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMIIYGR 300  
QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLGCGKERLKFGLCCHPFF 360  
DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLGCGKERLKFGLCCHPFF 360  
QY 361 SKIDMWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420  
DB 361 SKIDMWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

## RESULT 2

Q6XUH8 PRELIMINARY; PRT; 482 AA.

ID AC Q6XUH8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Citron Rho-interacting kinase short form.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mao Y., Xie Y., Wu Q.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AY209000; AAP43922.1; -  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000961; Kinase C.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002250; Ser\_Thr\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Kinase; I.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;

Query Match 93.2%; Score 2425; DB 2; Length 482;  
Best Local Similarity 98.9%; Pred. No. 3.4e-154;  
Matches 463; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
DB 1 MLKFKYGARNPSDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
QY 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
DB 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240  
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMIIYGR 300  
DB 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMIIYGR 300  
QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLGCGKERLKFGLCCHPFF 360  
DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLGCGKERLKFGLCCHPFF 360  
QY 361 SKIDMWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420  
DB 361 SKIDMWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

## RESULT 3

AAP43922 PRELIMINARY; PRT; 482 AA.

ID AAP43922;  
AC AAP43922;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Citron Rho-interacting kinase short form.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mao Y., Xie Y., Wu Q.;  
RL "Cloning and characterizing a novel human CR1K-SK gene."  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY209000; AAP43922.1; -  
KW Kinase.  
SQ SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;

Query Match 93.2%; Score 2425; DB 2; Length 482;  
Best Local Similarity 98.9%; Pred. No. 3.4e-154;  
Matches 463; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
DB 1 MLKFKYGARNPSDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120

QY 121 DIYAMKMKKALLAQEONVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 DB 121 DIYAMKMKKALLAQEONVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELIILAVSHVLMGYVHRDIKPNILVDRTGHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELIILAVSHVLMGYVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKNSNKNVNAKPIGTPTDYNAPVLTVMNGDGKGYGLDCDWSGVIAIYMIYGR 300  
 DB 241 GSAAKNSNKNVNAKPIGTPTDYNAPVLTVMNGDGKGYGLDCDWSGVIAIYMIYGR 300  
 QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
 DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKM 468

## RESULT 4

O88937 PRELIMINARY; PRT; 494 AA.  
 AC O88937;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Rho/rac-interacting citron kinase short isoform.  
 GN Name=Cit; Synonyms=Crik-sk;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99009084; PubMed=9792683;  
 RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,  
 RA Dotto G.P.;  
 RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase  
 RT encompassing the Rho-Rac-binding protein Citron.";  
 RL J. Biol. Chem. 273:29706-29711(1998).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF086823; AAC72822.1; -;  
 DR HSP; P31751; IGZK.  
 DR MGD; MGI:105313; Cit.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase-like.  
 DR InterPro; IPR000961; Kinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR02290; Ser\_thr\_pkinase.  
 DR InterPro; IPR08271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; Pkinase\_I.  
 DR Pfam; PF00433; Pkinase\_C.  
 DR Pfam; PF000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 494 AA; 55742 MW; 2C60D2294B28A185 CRC64;

Query Match 97.3%; Score 2271.5; DB 2; Length 494;  
 Best Local Similarity 97.3%; Pred. No. 6.8e-144;

Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;  
 QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFPGGPPFTQOQMSPLSGEILDALFVLFE 60  
 DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFPGGPPFTQOQMSPLSGEILDALFVLFE 60  
 QY 61 ECSQALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVVRKATG 120  
 DB 61 ECSQALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVVRKATG 120  
 QY 121 DIYAMKMKKALLAQEONVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 DB 121 DIYAMKMKKALLAQEONVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELIILAVSHVLMGYVHRDIKPNILVDRTGHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELIILAVSHVLMGYVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKNSNKNVNAKPIGTPTDYNAPVLTVMNGDGKGYGLDCDWSGVIAIYMIYGR 300  
 DB 241 GSAAKNSNKNVNAKPIGTPTDYNAPVLTVMNGDGKGYGLDCDWSGVIAIYMIYGR 300  
 QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
 DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVIFISAAGLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVIFISAAGLPCSR 480  
 QY 481 ILPSVYAKGSARGC 495  
 DB 480 ILQSIYAEAGSGAGHC 494  
 RESULT 5  
 O88938 PRELIMINARY; PRT; 2055 AA.  
 AC O88938;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Rho/rac-interacting citron kinase.  
 GN Name=Cit; Synonyms=Crik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99009084; PubMed=9792683;  
 RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,  
 RA Dotto G.P.;  
 RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase  
 RT encompassing the Rho-Rac-binding protein Citron.";  
 RL J. Biol. Chem. 273:29706-29711(1998).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF086824; AAC72823.1; -;  
 DR HSP; P31751; IGZK.  
 DR MGD; MGI:105313; Cit.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein...; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR005479; Cphp\_synth\_L\_D2.



```

RESULT 7
Q8AVM0
ID Q8AVM0 PRELIMINARY; PRT; 717 AA.
AC Q8AVM0
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cdc42bpb protein (Fragment).
GN Name=Cdc42bpb;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bonfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the Ser/thr protein kinase family.
DR EMBL; BC041741; AA041741.1; -.
DR HSP; P31751; IGZK.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 717
SQ SEQUENCE 717 AA; 83371 MW; 2D295D4A8A5B733A CRC64;

Query Match 35.7%; Score 929; DB 2; Length 717;
Best Local Similarity 41.7%; Pred. NO. 9.7e-54;
Matches 196; Conservative 84; Mismatches 148; Indels 42; Gaps 10;

QY 23 RASRLNLPFGKPPFTMQQMSPLSEGLDALFVLFECSQPALMKIKHNFV---RK 79
Db 6 RLKRLQLLDGP-----QRNEAVSVETLVDLLCLTCTSTLRDIYSEFEWAKP 61
QY 80 YSTIAELQELQPSAKDFEVRSLVGCCHFAEYVQVREKATGDIYAMKMKKALLAQEQV 139
Db 62 FTDL---LKGMLHRDDFEIKVIGRGAFGEVAVVLKSTERIYAMKILNKWMLKRAET 118
QY 140 SPFEERNILSRSTSPWIPOLQYAFQDKNHLVNMVEYQPGDLSILNRYEQLDENLIQ 199
Db 119 ACFREERNVLVNGDCQWITTLHYAFQDENLYLVMDYVVGDLTLTLKSFEDLPEDMSR 178
QY 200 FYLAELILAVSHVLMGYVHRDIKPENILVDRTGHIKLVDFGSAAMKSNKMNKAKLPTG 259
Db 179 FYLAEMVLAIHSIHQLHYVHRDIKPDNILLDMNGHRLADFGCLKMNKDGTVQSSVAVG 238
QY 260 TDDYVAPEVLTVNGDGKGTGDCDWSVGVIAMVEMIVYGRSPFAEGTSARTFNMMFQ 319
Db 239 TPDYISPEILOAME-DGMGKYGFECDMWSLGVCMYEMLYGETPFYAESLIVETYGKIMNHE 297
QY 320 RELKFPDD-PKYSDDFLDIQSLLCGOKERLKFEGL---CCHPFFSKIDMNNIRNSPPFF 375
Db 298 EFQFPFSGHIGDVSSEAKDLIQELICSRERRIQNGIDDFKAHPFEGIDWIRNLEAPY 357
QY 376 VPTLKSDDDTNFDPE---KNSVSSSPCQLSPSGEELPFVGFYSK-----423
Db 358 IPDVSSPSTSNFDVDDILRNPEIPSS---THSGFGFHPFVGVFTVTTDSCFSDRGS 414
QY 424 ----ALGILGRSESVSGLDSPAKTSMEKKL-----LKSKELQDS 461
Db 415 LKDTIHANAVTKDEDVQRLQNSLQVDAYERRIRLEQEKLELNRLQES 464

RESULT 8
Q6DT37
ID Q6DT37 PRELIMINARY; PRT; 1551 AA.
AC Q6DT37
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Myotonic dystrophy kinase-related CDC42-binding kinase gamma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ng Y., Tan I., Lim L., Leung T.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY648038; AAT67172.1; -.
SQ SEQUENCE 1551 AA; 172517 MW; 6B2DCED7BFE57B1E CRC64;

Query Match 35.7%; Score 929; DB 2; Length 1551;
Best Local Similarity 43.8%; Pred. NO. 2.6e-53;
Matches 184; Conservative 83; Mismatches 125; Indels 28; Gaps 7;

QY 49 EGILDALFVLFECSQPALMKIKHVSIVRKYSDTIAELQELQPSAKDFEVRSLVGCCHP 108
Db 23 DGLDLLLALHHELSLSSGFLRERSVAQFLSWASPFVSKVELRLQRDDFEILKVGAF 82
QY 109 AEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKN 168
Db 83 GEVTVVRQDITGQIFAMQMLHWEMLKRAETACFREEDVLVKGDSRWVTLHYAFQDEE 142

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Db 313 EDWVWSEAKDLIRQLICSSDVRFGRLGLSDPQLHPFFEGIDWNTIRSDNPPYVPEVSS 372
QY 382 DDDTSNFDPEKNSWSSSPC--QLSP---SGFSGEELPFVGFYSKALGILGRSESV 435
Db 373 PETSINFDVDCBD--DFTPCLOETOPRVLAAFTGNHLPFVGFYSHTG--SLSDARSUT 429
QY 436 SGLDSPAKTSSMEKLLIKS 455
Db 430 DEIRATAQRCCGDAELMEKS 449

RESULT 11
Q86X28 PRELIMINARY; PRT; 492 AA.
ID Q86X28 AC Q86X28;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE CDC42BPB protein (Fragment).
GN Name=CDC42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC048261; AAH48261.1; -.
DR HSSP; P31751; 1GZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 492
SQ SEQUENCE 492 AA; 59580 MW; 59FBD9CC1D2ABFC CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 492;
Best Local Similarity 42.1%; Pred. No. 9.1e-52;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQLQPSAKDFEVSUV 103
Db 23 SALSVELLLDLVCLYTECSHSALRDKYVAEFLWAKPFTQLVKEMQLHREDFEIKVI 82
QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQBQVSVFFEEERNILSRSTSPWIPOLQYA 163
Db 83 GRGAFGEVAVVVMKQNTERRIYAMKILNKWEMLKRAETACFREERDLVNGDCQITAHYA 142
QY 164 FQDKNHLVLMYQPGDGLLSLNRYEDQDENLIQIYLAELILAVHSVHLMGYVHRDIK 223
Db 143 FQDENHLVLMYDYYVGGDLTLTLLSKFEDKLPEDMARFYIGEMVLADSIHQHLYVHRDIK 202
QY 224 PENILVPTGHIKLVDGSAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGGKTYGLD 283
Db 203 PDNVLLDVGHIRLADFGSLKMDNDGTQVSSVAVGPDYISFEILOAMP--DMGKXGPE 261
QY 284 CDWMSVGVIAYEMTYGRSPFAEGTSARTFNMINMFORFLXFPDD--PKVSSDFDLDIQSL 342
Db 262 CDWMSLGVCMYEMLYGETPFVAESLVETYGKIMHBERFOFPSSHVTDVSEAKDLIQLRI 321
QY 343 CGQKERLKEFGL---CHPFFSKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEPE---KNSW 396
Db 322 CSRRLRQNGIEDFKHAFTEGLNWINIRLEAPYIPDVSSPSDYSNFDVDDVLRLNTE 381
QY 397 VSSSPCQLSP---SGFSGEELPFVGFYSKALGILGRSESVSGLDSPAKTSSMEKLLI 453
Db 392 I-----LPPGSHTGFGSLHLPFGIFT-----TESCFs--DRGSLKSIQSNLT 425
QY 454 KSKLQDSQDKCHKVF-SA 472
Db 426 KDEVDQ--RDLEHSLQMEA 442

RESULT 12
Q86TJ1 PRELIMINARY; PRT; 933 AA.
ID Q86TJ1 AC Q86TJ1;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE CDC42BPB protein (Fragment).
GN Name=CDC42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC048261; AAH48261.1; -.
DR HSSP; P31751; 1GZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; BC047871; AAH47871.1; --  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000961; Kinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TK\_X; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 FT NON TER 933  
 SQ SEQUENCE 933 AA; 108543 MW; 38E7179C3253F521 CRC64;  
 Query Match 34.5%; Score 896.5; DB 2; Length 933;  
 Best Local Similarity 42.1%; Pred. No. 2e-51;  
 Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;  
 QY 44 SPLREGILDALFVLFECSSQALMKIKHVSFVKYSDTIAELQELQPSAKDFEVSRLV 103  
 DB 23 SALSVEILLDLVLCYTECHSALRRDKYVAEFLWAKPTQLVKEMQLHREDFEIKVI 82  
 QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163  
 DB 83 GRGAFGEVAVVMKNTIRIYAMKILNKWMLKRAETACFREERDVLVNGDCQWITALHYA 142  
 QY 164 FQDKNHLVLMVEYQGGDLISLNRYEDQDENLIQFYLAELILAVSHVLMGVYHRDIK 223  
 DB 143 FQDENHLYLVMDYVYVGGDLTLTKSKFEDKLPEDMARFYIGEMVLAIIDSIHQLHYVHRDIK 202  
 QY 224 PENLLVDRTHIKLIVDFGSAKNSKNSKWNNAKLPIGTDPYMAPEVLTVNMGDKGYGLD 283  
 DB 203 PDNVLLDVNGHIRLADFGSLCKNNDGTVOSSVAVGTPDIISPEILQAME-DNGKYGPE 261  
 QY 284 CDWWSGVVIAYEMLYGRSPAGTSARTFNINMNFQRLKPPD-PKVSSDFDLQLQSLL 342  
 DB 262 CDWWSLGVCMYEMLYGETPYAESLVEYTKIMNHERFQPSHVTDVSEAKDLIQRLLI 321  
 QY 343 CGOKERLKFGL---CCHPFESKLDNNIENSPPFPVPTLKSDDDTSNDEPE---KNSW 396  
 DB 322 CSRRRLQGQIEDFKKHAFEGELNWNIRNLKAPYIPDVSSPSDTSNFDVDDVLRNTE 381  
 QY 397 VSSSPCOLSP---SGFSGEELPFVGFYSKALGILGRSESVWGLDSPAKTSMKELLI 453  
 DB 382 I-----LPGSHGTGFGSLHLPFGTFTT-----TESCFs--DRGSLKSIQNTLIT 425  
 QY 454 KSKELQSQDKCHKVFISA 472  
 DB 426 KBDVQ--RDLEHSLQMEA 442  
 PRELIMINARY; PRT; 1711 AA.

RESULT 13

Q9Y5S2

ID Q9Y5S2

AC Q9Y5S2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CDC42-binding protein kinase beta.  
 GN Name=CDC42BPA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Brain;  
 RX MEDLINE=99216425; PubMed=10198171;  
 RA Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;  
 RT "Cloning and chromosomal localization of human Cdc42-binding protein  
 RT kinase beta.";  
 RL Genomics 57:297-300 (1999).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF128625; AAD37506.1; --  
 DR HSSP; P31751; 1GZK.  
 DR GO; GO:0005856; C:cytoskeleton; TAS.  
 DR GO; GO:0004672; F:protein kinase activity; TAS.  
 DR GO; GO:0007163; P:establishment and/or maintenance of cell po. .; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR002219; DAG PE-bind.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000095; PAKbox/RhoBindg.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00130; C1\_1; 1.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00786; PED; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR PRINTS; PR00008; DAGPEDOMAIN.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00036; CNH; 1.  
 DR SMART; SM0285; EBD; 1.  
 DR SMART; SM0233; PH; 1.  
 DR SMART; SM00220; S\_TK\_X; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS0108; CRTB; 1.  
 DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.  
 DR PROSITE; PS00081; DAG PE BIND DOM 2; 1.  
 DR PROSITE; PS00003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1711 AA; 194356 MW; 3A3731D40A363497 CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 1711;  
 Best Local Similarity 42.1%; Pred. No. 4.4e-51;  
 Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPLREGILDALFVLFECSSQALMKIKHVSFVKYSDTIAELQELQPSAKDFEVSRLV 103  
 DB 23 SALSVEILLDLVLCYTECHSALRRDKYVAEFLWAKPTQLVKEMQLHREDFEIKVI 82  
 QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163  
 DB 83 GRGAFGEVAVVMKNTIRIYAMKILNKWMLKRAETACFREERDVLVNGDCQWITALHYA 142  
 QY 164 FQDKNHLVLMVEYQGGDLISLNRYEDQDENLIQFYLAELILAVSHVLMGVYHRDIK 223  
 DB 143 FQDENHLYLVMDYVYVGGDLTLTKSKFEDKLPEDMARFYIGEMVLAIIDSIHQLHYVHRDIK 202

QY 224 PENILVDRTHGHIKLVDFGSAKNSKRVNNAKLPIGTPDYMAPEVLTVNMGDKGKTYGLD 283  
 Db 203 PDNVLLDVNGHIRLADFGSLKXNDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 261  
 QY 284 CDWWSGVGVIAEMMYGRSPAEAGTSARTFNINMFORFLKFPDD-PKUSDFDLIQLSL 342  
 Db 262 CDWWSLGVGVIAEMMYGRSPAEAGTSARTFNINMFORFLKFPDD-PKUSDFDLIQLSL 321  
 QY 343 CGOKERLKPGL---CCHPFPSKIDMNNIRNSPPFVPTLKSDDDTSNFEPE---KNSW 396  
 Db 322 CSERRLQNGIEDFKHAFEGELNENIRNLEAPIDVSSPSDSINFEVDVDDVLRNTE 381  
 QY 397 VSSSPQQLSP---SGFSGEELPFVGFYSYKALGILGRSSVSGLDSPAKTSMEKKLLI 453  
 Db 382 I-----LPPGSHGTGSLHLPIGTFIT-----TESCFS--DRGSLKSIQSNLT 425  
 QY 454 KSKELQDSQDKCHKVFISA 472  
 Db 426 KDEDVQ--RDLEHSLQMEA 442

RESULT 14

Q99646 PRELIMINARY; PRT; 1760 AA.

AC Q99646  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE KIAA1124 protein (Fragment).  
 GN Name=KIAA1124;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP TISSUR=Brain;  
 RC MEDLINE=20039618; PubMed=10574461;  
 RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;  
 RT "Characterization of cDNA clones selected by the GeneMark analysis  
 from size-fractionated cDNA libraries from human brain."  
 RL DNA Res. 6:329-336(1999).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR ENBL; AB032950; BA86438.2;  
 DR Genew; HGNC:1738; CDC42BPB.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR011009; Kinase-like.  
 DR InterPro; IPR000095; PAXbox/Shobndng.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00130; Cl\_1; 1.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR PRINTS; PR00008; DAGPEDOMAIN.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00109; Cl; 1.  
 DR SMART; SM00036; CNH; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00220; S\_TKX; 1.  
 DR SMART; SM00133; S\_TKX; 1.

DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS00003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 1760 AA; 199208 MW; 3A1CA9A7A4BF5FA3 CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 1760;  
 Best Local Similarity 42.18; Pred. No. 4.5e-51;  
 Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPLREGILDALFVFECSOPALMKIKHVSNFVRKYSDTIALQELQPSAKDFEVSRLV 103  
 Db 72 SALSVETLLDVLCVTECSHSLRRDKYVAEFLWAKPFTQLVKEMQLHREDFEIKVI 131  
 QY 104 GCGHFAEVQVVRKATGDIYKVMKKKALLAEOVSFFEEERNILSRSTSPWIPOLQYA 163  
 Db 132 GRGAFGEVAVVVMKNTIRIYAMKILNKWEMLKRAETACFREERDVLVNGCQWITALHYA 191  
 QY 164 PQKNHLYVMYQPGGDLNRYEDQDENLQFYLAELILAVHSHVMGYVHRDIK 223  
 Db 192 QDENHLYVMYVGGDLTLLSKFEDKLPEDVAREFYIGEMVLADSIHQLHYVHRDIK 251  
 QY 224 PENILVDRTHGHIKLVDFGSAKNSKRVNNAKLPIGTPDYMAPEVLTVNMGDKGKTYGLD 283  
 Db 252 PDNVLLDVNGHIRLADFGSLKXNDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 310  
 QY 284 CDWWSGVGVIAEMMYGRSPAEAGTSARTFNINMFORFLKFPDD-PKUSDFDLIQLSL 342  
 Db 311 CDWWSLGVGVIAEMMYGRSPAEAGTSARTFNINMFORFLKFPDD-PKUSDFDLIQLSL 370  
 QY 343 CGOKERLKPGL---CCHPFPSKIDMNNIRNSPPFVPTLKSDDDTSNFEPE---KNSW 396  
 Db 371 CSERRLQNGIEDFKHAFEGELNENIRNLEAPIDVSSPSDSINFEVDVDDVLRNTE 430  
 QY 397 VSSSPQQLSP---SGFSGEELPFVGFYSYKALGILGRSSVSGLDSPAKTSMEKKLLI 453  
 Db 431 I-----LPPGSHGTGSLHLPIGTFIT-----TESCFS--DRGSLKSIQSNLT 474  
 QY 454 KSKELQDSQDKCHKVFISA 472  
 Db 475 KDEDVQ--RDLEHSLQMEA 491

RESULT 15

Q99646 PRELIMINARY; PRT; 496 AA.

AC Q99646  
 DT 01-MAY-1997 (TREMELrel. 03, Created)  
 DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Ser-thr protein kinase PK428.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. Kraft A.S.;  
 RA Zhao Y., Kidd V., Kraft A.S.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR ENBL; U59305; AAB37126.1; -.  
 DR HSSP; P31751; 1GZK.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR InterPro; IPR011009; Kinase-like.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.

Search completed: November 8, 2004, 12:31:34  
Job time : 198 secs

Search completed: November 8, 2004, 12:31:34  
Job time : 198 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 12:22:26 ; Search time 41 Seconds  
(without alignments)  
1166.335 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKFKYGARNPLDAGAEPI.....CSRILPSVYAKSGARGCWL 497  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 791.\*

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908.5	34.9	1548	2 T25808	hypothetical prote
2	891	34.2	1732	2 T14039	protein kinase (EC
3	883	33.9	1702	2 T14050	protein kinase (EC
4	876.5	33.7	1173	2 T25539	hypothetical prote
5	866.5	33.3	1354	2 S74244	serine/threonine-s
6	864.5	33.2	1354	2 S69211	serine/threonine-s
7	863	33.2	624	2 B49364	protein kinase (EC
8	860.5	33.1	1388	2 S70333	serine/threonine-s
9	853.5	32.8	1388	2 S74245	serine/threonine-s
10	847	32.6	557	2 S71829	serine/threonine-s
11	721	27.7	522	2 G86431	protein kinase T51
12	711	27.3	479	2 S42864	protein kinase (EC
13	704	27.1	756	2 S60966	probable protein k
14	701	26.9	526	2 S49077	protein kinase PKT
15	700	26.9	469	2 T41723	serine/threonine-s
16	697	26.8	596	2 F84589	probable protein k
17	693	26.6	509	2 A86170	hypothetical prote
18	687.5	26.4	474	2 I78396	myotonic dystrophy
19	685	26.3	441	2 I78393	myotonic dystrophy
20	685	26.3	516	2 I78394	myotonic dystrophy
21	682.5	26.2	1356	2 T16718	hypothetical prote
22	676.5	26.0	443	2 D71405	probable protein k
23	676.5	26.0	475	2 H85156	protein kinase [im
24	674.5	25.9	465	2 I38133	protein kinase (EC
25	665.5	25.6	500	2 S42867	protein kinase (EC
26	660.5	25.4	483	2 T05188	protein kinase F41
27	639	24.6	545	2 T01288	protein kinase F27
28	636.5	24.5	598	2 T47254	serine/threonine k
29	636.5	24.5	685	2 S70706	probable protein k

30	636	24.4	480	2 T47255	serine/threonine k
31	636	24.4	620	2 S22711	probable protein k
32	608	23.4	908	2 T25035	hypothetical prote
33	606.5	23.3	412	2 I78395	myotonic dystrophy
34	604	23.2	1099	2 A56155	tumor suppressor p
35	548	21.1	607	2 S62556	probable serine/th
36	536	20.6	624	2 T41341	probable serine-th
37	532.5	20.5	564	2 S59776	protein kinase DAF
38	522	20.1	572	2 S64387	protein kinase DBF
39	520.5	20.0	726	2 S22258	probable protein k
40	520	20.0	1092	2 H96509	protein F27F5.23 l
41	516	19.8	893	2 S63378	hypothetical prote
42	515	19.8	425	2 S41099	protein kinase (EC
43	510.5	19.6	646	2 T38171	probable serine/th
44	510	19.6	462	1 T17287	protein kinase (EC
45	509	19.6	569	2 T50414	probable prolifera

ALIGNMENTS

RESULT 1

T25808  
hypothetical protein K08B12.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004  
C;Accession: T25808  
R;Becker, M.; Wohldmann, P.  
submitted to the EMBL Data Library, April 1997  
A;Description: The sequence of C. elegans cosmid K08B12.  
A;Reference number: Z20091  
A;Accession: T25808  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1548 <BEC>  
A;Cross-references: UNIPROT:O01583; EMBL:U97001; PIDN:AAB52260.1; GSPDB:GN00023; CESP:K  
A;Experimental source: strain Bristol N2; clone K08B12  
C;Genetics:  
A;Gene: CESP:K08B12.5  
A;Map position: 5  
A;Introns: 39/1; 66/1; 156/3; 278/2; 391/3; 628/1; 1022/2; 1273/3; 1326/1; 1423/2; 1489/2; 1489/2  
C;Superfamily: protein kinase homology  
F;956-1005/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match	34.9%	Score	908.5	DB	2	Length	1548
Best Local Similarity	40.6%	Pred. No.	2.3e-33				
Matches	178	Conservative	91	Mismatches	150	Indels	19
Gaps	7						
Qy	28	NLFQGGKPPFTMTQQQMSPLSREGILDALFVLFECSSQALMKIKHVSNNFVKYSDTIAEL	87				
Db	19	NIYMDG-----PSKPEALSFETLDSLCYDECCNSTLRKEKCIAEFFSVSKTVISKA	73				
Qy	88	QELPSAKDFEVRSLVGGCHFAEQVVRKATGIYAKVMKKKALLAQEQVFFEEBEN	147				
Db	74	KRLSRDDFEVLKVIKGAFGEVAVVMRGVGIYAKMILNKWVKRAETACFRERD	133				
Qy	148	ILSRSTSWIQLQYAFQDKNHLVLMVEYQGGDLLSLNRYEDOLDENLQFYLAELIL	207				
Db	134	VLVYGDREWIINLHYAFQDEKNLYFVMDYIYGGDMLTLLSFVDHPIESMAKFIYAENVL	193				
Qy	208	AVHSHLMGYVHRDIKPNILVDRTGHIKLVDFGSAAMKNSKMNKAKLPTGTDYMAPE	267				
Db	194	AIDSLHRJGVYHRDVKPDNVLDMQGHRLADFGSCLRLADGVSASNVAVGTDPDYISPE	253				
Qy	268	VLTVMNGKGKTYGLDCDWSVGVIAYEMIVGRSPFAGTSAFTNNINNFQFLKFPDD	327				
Db	254	ILRAME-DGRGYGKECDWNSLIGICMVELYGTTPFYSERLVDTIVYKIMSHQDMLDFPDD	312				
Qy	328	P---KVSSDFDLDTLSLTCGQKERLKPGLC---CHPFFSKIDWNININSPPPFVPTLKS	381				
Db	313	EIDWVVSSEAKDLRLQLICSSDVFGRNGLSDFLHPFFEGIDWNTIRDSNPPFVPEVSS	372				
Qy	382	DDTNSFNDEPKNSWSSSPCQLSP----SGFSGEELPFVGFYSKALGILGRSESVVSG	437				

Db 373 PEDTSNFDVDCBD--DFTPCETQPPRVLAFAFTGNHLPVGFYSYTHG-SLLSDARSLATDE 429  
QY 438 LDSPAKTSSEKELLKS 455  
Db 430 IRAIAQRCOGDAELMEKS 447

## RESULT 2

Tl4039  
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: Tl4039  
R;leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.  
Mol. Cell. Biol. 18, 130-140, 1998  
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector  
A;Reference number: 217862; MUID:98078670; PMID:9418861  
A;Accession: Tl4039  
A;Status: preliminary; translated from GE/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1732 <LEU>  
A;Cross-references: UNIPROT:O54874; EMBL:AF021935; NID:g2736150; PID:g2736151; PIDN:AAC02  
C;Genetics:  
A;Gene: MRCK  
C;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;75-343/Domain: protein kinase homology <KIN>  
F;1013-1062/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 34.2%; Score 891; DB 2; Length 1732;  
Best Local Similarity 40.3%; Pred. No. 1.5e-32;  
Matches 183; Conservative 91; Mismatches 146; Indels 34; Gaps 8;

QY 36 PFMTQOQMSPLSREGILDALFVLFECSPALMKIKHVSFVRKYSDTIAELQELQPSAK 95  
Db 18 PAQTNGQC--FSVETLLDILICLYDCNNSPLRRKNIYLELWAKPFTSKVKQMLHRE 75  
QY 96 DFEVRLVGGCHFAEVQVREKATGDIYAMKVMKKALLAQEQVSFFEEERNILSRSTSP 155  
Db 76 DFEILKVIKRGAFGEVAVVKLNADKVFAMKILNKWMLKRAETACFREERDLVNGDSK 135  
QY 156 WIPOLQAFODKXHLVMEYQPGDGLLSLNRYEDQDENLIOFYLAELILAVHSVHLM 215  
Db 136 WITLHYAFODDNNILVMDYYVGGDLTLTSKFDRLPEEMARFYLAEMVLAIDSVHOL 195  
QY 216 GYVHRDIKPNILVDRTHGHLKLVDFGSAAKNSKNVNAKLPIGTPDYMAPEVLTVMGD 275  
Db 196 HYVHRDIKPNILMDNMKGHRLADFGSLKMBDGTQVSSVAVGTPDYISPILQAME-D 254  
QY 276 GKTYGLDCDWVGVYAVEMVYGRSPFAEGTSARTFNINMFORFLKFPDD-PKVSSDF 334  
Db 255 GKRGYGECDWNLGVCVMEYLGTPFYAESLVETYGKIMNHEERFQFPQTQVTVSENA 314  
QY 335 LDLIQSLCQKRLKEFLG---CCHPFFSKIDNNIRNSPPFPVTLKSDDDTSNFDPEP 391  
Db 315 KDLIRLILCSREHRLQNGIEDPKHFFTSFGIDWNIRNCEAPYIPEVSSPTDSNFDVD 374  
QY 392 E---KNSWSSSCQLSPSGFSGEELPFVGFYSKALGILGS-----ESV 434  
Db 375 DCLKNSETNPP---THTAFSGHLLPFVGFYTTSSCVLSDRSCLRVTAGTSLDLVDNV 431  
QY 435 VSGLDSPAKTSSEKKL-----LIKSELODS 461  
Db 432 QRTLDNNLATEAVERRIKLEQELKLETRKLQES 465

## RESULT 3

Tl4050  
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: Tl4050

R;leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.  
Mol. Cell. Biol. 18, 130-140, 1998  
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector  
A;Reference number: 217862; MUID:98078670; PMID:9418861  
A;Accession: Tl4050  
A;Status: preliminary; translated from GE/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1702 <LEU>  
A;Cross-references: UNIPROT:O54875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AAC02  
C;Genetics:  
A;Gene: MRCK-beta  
C;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;74-342/Domain: protein kinase homology <KIN>  
F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.9%; Score 883; DB 2; Length 1702;  
Best Local Similarity 40.5%; Pred. No. 3.4e-32;  
Matches 182; Conservative 90; Mismatches 139; Indels 38; Gaps 9;

QY 44 SPLSREGILDALFVLFECSPALMKIKHVSFVRKYSDTIAELQELQPSAKFEVRSLV 103  
Db 23 SLSVETLLDVLVCLYTECSHSLRRDKYVAEFLWAKPFTQLVKQMLHREDFEIKVI 82  
QY 104 GCGHFAEVQVREKATGDIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163  
Db 83 GRGAFGEVAVVKMKNTERIYAMKILNKWMLKRAETACFREERDLVNGDCQWITALHYA 142  
QY 164 PQDKXHLVMEYQPGDGLLSLNRYEDQDENLIOFYLAELILAVHSVHLMGYVHRDIK 223  
Db 143 FQDENYILVMDYYVGGDLTLTSKFDRLPEEMARFYIGEMVLADSITQLHYVHRDIK 202  
QY 224 PENILVDRTHGHLKLVDFGSAAKNSKNVNAKLPIGTPDYMAPEVLTVMGDCKGTG 283  
Db 203 PDNVLVDVNGHRLADFGSLKMBDGTQVSSVAVGTPDYISPILQAME-DGMKYGPE 261  
QY 284 CDWMSGVYAVEMVYGRSPFAEGTSARTFNINMFORFLKFPDD-PKVSSDFDLDIQSL 342  
Db 262 CDWNLGVCVMEYLGTPFYAESLVETYGKIMNHEERFQFPQSHVTDVSEAKDLIOLRI 321  
QY 343 CGQKRLKEFLG---CCHPFFSKIDNNIRNSPPFPVTLKSDDDTSNFDPEP---KNSW 396  
Db 322 CSRRRLQNGIEDPKHFFTEGLNENIRNLEAPYIPDVSPSPDTSNFDVDVLRNIE 381  
QY 397 VSSSPCOLSP---SGFSGEELPFVGFYS-----KAL---GILGRSSVVSGLD 439  
Db 382 I-----LPPGSHGTGSLHLPFGITFTTESCFSDRGSLSKMSIQSNLTITKDEVDVORDLE 435  
QY 440 SPAKTSSEKKL-----LIKSELODS 461  
Db 436 NSLQIEAVERRIKLEQELKLETRKLQES 464

## RESULT 4

T25539  
hypothetical protein Cl0H11.9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T25539  
R;Dante, M.; Wamsley, P.  
submitted to the EMBL Data Library, February 1997  
A;Description: The sequence of C. elegans cosmid Cl0H11.  
A;Reference number: Z20047  
A;Accession: T25539  
A;Status: preliminary; translated from GE/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1173 <DAN>  
A;Cross-references: UNIPROT:P92199; EMBL:U08311; PIDN:AAB42348.1; GSPDB:GN00019; CESP:CL0H11  
A;Experimental source: strain Bristol N2; clone Cl0H11  
C;Genetics:  
A;Gene: CESP:Cl0H11.9  
A;Map position: 1



A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 865/3; 891/3; 970/3; 1027/3; 1114/1  
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology

Query Match 33.7%; Score 876.5; DB 2; Length 1173;  
Best Local Similarity 40.9%; Pred. No. 4.7e-32;  
Matches 169; Conservative 88; Mismatches 142; Indels 13; Gaps 6;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 15 SPINISLLDTITALVNDCKIPVLMRMKSVDFNISRYERWVESLAALRMKAADFRLQKVI 74

QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPQLOYA 163  
DB 75 GRGAFGEVHLVRTRINTVTAMKMKDDMIKADSAFFWEERDINAHANSEWVRLQYA 134

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIK 223  
DB 135 FQDPRHLYMWEYMPGDLVNLTSYE--VSEKWTFYTAIEIVALEAALSHMGYIHRDVK 192

QY 224 PENILVDRTHIKLVDFGSAAKNSNMVNNAKLPITGPDYMAPEVLTVMGDKGTYGLD 283  
DB 193 PDNNLISISGHILKADFGTCVMKANGVRCSTAVGTPDYISPEVLRNQGDAE--FGKE 250

QY 284 CDWMSVGVIAEMVIGRSPFAEGTSARTFNINMNFQRLKFPDPKPVSSDFDLIQSLLC 343  
DB 251 VDWMSVGVPIYELVGETFYAEALVSTYINMNHKTSLKFPDEPLISTQAKDIKKFLS 310

QY 344 GQKERL---KFEGLCHPFFSKIDN--NIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 311 AAPDLGRNSVDDIRNHKFFVNDWTFATLREASPPVIFSLKSDDDTTFEBIETRDRN 370

QY 399 SSPCOLSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSMEK 449  
DB 371 AGDFQL-PKTFNGQLPFGFTYSNYSVPV---KNLLRGHGAGSKONGIEQ 417

RESULT 5  
S74244  
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 16-Aug-2004  
C;Accession: S74244  
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.  
FEB5 Lett. 392, 189-193, 1996  
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein  
A;Reference number: S74244; MUID:96368048; PMID:8772201  
A;Accession: S74244  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1354 <NAK>  
A;Cross-references: UNIPROT:P70335; EMBL:U58512; NID:g1514695; PID:AAC53132.1; PID:g1514695  
C;Keywords: coiled coil; phosphotransferase; protein kinase homology  
F;74-338/Domain: protein kinase homology <KIN>  
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.3%; Score 866.5; DB 2; Length 1354;  
Best Local Similarity 40.0%; Pred. No. 1.5e-31;  
Matches 186; Conservative 93; Mismatches 157; Indels 29; Gaps 10;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 23 SEVNSDCLLDGLDALVYDLDFPALRKKNKIDNFLSRKYDKTINKIRDLRMKAEDYEVVKVI 82

QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPQLOYA 163  
DB 83 GRGAFGEVQLVRHKSTRKYAMKLLSKFEMIKSDSAFFWEERDINAFANSPWVQLFYA 142

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIK 223  
DB 143 FQDPRHLYMWEYMPGDLVNLMSNYD--VPEKWARFYTAIEVLALDAISHMGFIHRDVK 200

QY 224 PENILVDRTHIKLVDFGSAAKNSNMVNNAKLPITGPDYMAPEVLTVMGDKGTYGLD 283  
DB 201 PDNNLDSKSHGLKADFGTCVMKANGVRCSTAVGTPDYISPEVLSKQSGD--GYYGRE 258

QY 284 CDWMSVGVIAEMVIGRSPFAEGTSARTFNINMNFQRLKFPDPKPVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFIYELMVGDTTPFYADSLVGYTSKIMNHKNSLTFFDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKFEG---LCCHPFFSKID--WNIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRNGRVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSSDIDTSNFDDEEDKGE 378

QY 399 SS-PCQLSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSME--KULLIKS 455

DB 201 PDNNLDSKSHGLKADFGTCVMKANGVRCSTAVGTPDYISPEVLSKQSGD--GYYGRE 258

QY 284 CDWMSVGVIAEMVIGRSPFAEGTSARTFNINMNFQRLKFPDPKPVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFIYELMVGDTTPFYADSLVGYTSKIMNHKNSLTFFDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKFEG---LCCHPFFSKID--WNIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRNGRVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSSDIDTSNFDDEEDKGE 378

QY 399 SS-PCQLSPGFSGEELPFVGFYSKALGILGRSESVV--SGLDSPAKTSSME 448  
DB 379 ETFEPI--PKAFVGNQLPFPVGFYTSNRRYLPSANSENSSNVKSLQESLQKTIYKL 435

QY 449 KKLILKSKELQDS--QDKCHKVFISAAGLLPCSRILPSVYAKGSAR 492  
DB 436 EQULHNEQLKDEMEQKCR-----TSNKLKDKIMKELDEEGNQR 474

RESULT 6  
S69211  
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 16-Aug-2004  
C;Accession: S69211; S71910  
R;Ishizaki, T.; Maekawa, M.; Fujisawa, K.; Okawa, K.; Iwanatsu, A.; Fujita, A.; Watanabe  
EMBO J. 15, 1885-1893, 1996  
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot  
A;Reference number: S69211; MUID:96203110; PMID:8617235  
A;Accession: S69211  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1354 <SHL>  
A;Cross-references: UNIPROT:Q13464; EMBL:U43195; NID:g1276900; PID:AA802814.1; PID:g1276900  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;74-338/Domain: protein kinase homology <KIN>  
F;82-90/Region: protein kinase ATP-binding motif  
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.2%; Score 864.5; DB 2; Length 1354;  
Best Local Similarity 41.1%; Pred. No. 1.8e-31;  
Matches 180; Conservative 89; Mismatches 146; Indels 23; Gaps 9;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 23 SEVNSDCLLDGLDALVYDLDFPALRKKNKIDNFLSRKYDKTINKIRDLRMKAEDYEVVKVI 82

QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPQLOYA 163  
DB 83 GRGAFGEVQLVRHKSTRKYAMKLLSKFEMIKSDSAFFWEERDINAFANSPWVQLFYA 142

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIK 223  
DB 143 FQDPRHLYMWEYMPGDLVNLMSNYD--VPEKWARFYTAIEVLALDAISHMGFIHRDVK 200

QY 224 PENILVDRTHIKLVDFGSAAKNSNMVNNAKLPITGPDYMAPEVLTVMGDKGTYGLD 283  
DB 201 PDNNLDSKSHGLKADFGTCVMKANGVRCSTAVGTPDYISPEVLSKQSGD--GYYGRE 258

QY 284 CDWMSVGVIAEMVIGRSPFAEGTSARTFNINMNFQRLKFPDPKPVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFIYELMVGDTTPFYADSLVGYTSKIMNHKNSLTFFDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKFEG---LCCHPFFSKID--WNIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRNGRVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSSDIDTSNFDDEEDKGE 378

QY 399 SS-PCQLSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSME--KULLIKS 455



QY 426 GILGRSBSVSGLDSPA--KTSSMEKKLLIKSKELQDSQDKCH 466  
DB : : : : :  
DQ : : : : :  
Bb 420 LLAS-----DSPCKENDSIQSR---KNEESQEIQKKLY 450

RESULT 9  
S74245

C:serine/threonine-specific protein kinase (EC 2.7.1.-) isoform II, Rho-associated - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 16-Aug-2004  
C:Accession: S74245  
R:Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saico, Y.; Nakao, K.; Narumiya, S.  
FEBS Lett. 392, 189-193, 1996  
A>Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein  
A:Reference number: S74244; MJTD:96368048; PMID:8772201  
A:Accession: S74245  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1388 <NA>  
A:Cross-references: UNIPROT:P70336; EMBL:U58513; NID:G1514697; PIDN:AAC53133.1; PID:g1514697  
C:Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology  
C:Keywords: phosphotransferase, serine/threonine-specific protein kinase  
F:90-354/Domain: protein kinase homology <KIN>  
F:1361-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 32.8%; Score 853.5; DB 2; Length 1388;  
Best Local Similarity 40.08; Pred. No. 5.7e-31;  
Matches 177; Conservative 95; Mismatches 144; Indels 27; Gaps 9;

QY 32 QGKPPFTQQMSPLRGEGILDALFVLFEBCSPALMKIKHVSFNFKYSDDTAEQLQL 91  
DB : : : : :  
DQ : : : : :  
Bb 27 QRKLEAIRDRPFINVESLDGLNSLVLDLPFAURKNKNIDNFLNRVEKIYVKIRGLQ 86

QY 92 PSADPEVRSLVGCGHFAEYQVVREKATGDIVAMKVWKKALLAQEQVSFFEEERILSR 151  
DB : : : : :  
DQ : : : : :  
Bb 87 MKAEEDYDVVKVIKGAFGEQVLRHRKASQKYANKLLSFEMIKRSDSAFFWEERIMAF 146

QY 152 STSPWPLOIYAFQDNKHLYLVNEYQPGDLLSLNRYEDOLDENLIQFYLAELIIAVHS 211  
DB : : : : :  
DQ : : : : :  
Bb 147 ANSPWVQLFCAPQDDRXYLVVMYMPGGDLVNLMSNYD--VPEKWAKPYTAEVWLALDA 204

QY 212 VHLMGVYVHRDIKPENITLVDRTHGIKLVDGSAARKSNKYNKAKLPITGYDYMAPEVLTV 271  
DB : : : : :  
DQ : : : : :  
Bb 205 IHSXGLIHDRVDPNNMLLKHGHLKLADRGTCKMMDETGMVHCOTAVTGPDYISPEVLKS 264

QY 272 MNGDGKTYGLCDWMWSGVYAYEMIYGRSPFAEGTSARTFNMINMFQRFLKFPDPPKYS 331  
DB : : : : :  
DQ : : : : :  
Bb 265 QGGD--GYYGRCEDMWMSGVFELFMELVGDTPFYADSVLGVTYSKIMDHKNSCLCFPEDTELS 322

QY 332 SDFLDLTIQSILCOGERLAFEG---LCCHPFPSKIWN--NTRNSSPPFPPTLKSDDDTS 386  
DB : : : : :  
DQ : : : : :  
Bb 323 KIAXNLICAFLTDTREVRLGRNGVVEIKQHFFPKNDQMNWDNIETAAPVVPVELSSIDDSS 382

QY 387 NFDEPEPKNSW-VSSSPQCQLSPGSFGSEELPFVFGYSYKALGILGRSESUVSGLDSP--AK 443  
DB : : : : :  
DQ : : : : :  
Bb 383 NFDDIEDKGDVETTFPI---PRAFVGNQLPFIGTTYFRENLLS-----DSPCKRE 430

QY 444 TSSEMEKKLLIKSKELQDSQDKCH 466  
DB : : : : :  
DQ : : : : :  
Bb 431 NDAIQT---KSEESOIEOKKLY 450

RESULT 10  
S71829  
serine/threonine-specific protein kinase (EC 2.7.1.1.) - mouse  
N;/Alternate names: myotonic dystrophy-associated protein kinase; myotonin protein kinase  
C;/Species: Mus musculus (house mouse)  
C;/Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 16-Aug-2004  
C;/Accession: S71829, S38815  
R;/Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Worth  
submitted to the EMBL Data Library, January 1993  
A;/Description: Structure and genomic sequence of the myotonic dystrophy kinase (DM kinase)

A:Reference number: S71829  
A:Accession: S71829  
A:Molecule type: DNA  
A:Residues: 1-557 <MAH>  
A:Cross-references: UNIPROT:P54265; EMBL:Z21505  
R:Mahadevan, M.S.; Anemiyva, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Hum. Mol. Genet. 2, 299-304, 1993  
A:Title: Structure and genomic sequence of the myotonic dystrophy (DM kinase) gene.  
A:Reference number: S38815; MUID:93271990; PMID:8499920  
A:Accession: S38815  
A:Molecule type: DNA  
A:Residues: 1-53 <MAW>  
A:Cross-references: EMBL:Z21503  
C:Genetics:  
A:Introns: 54/1; 84/3; 112/3; 144/3; 194/2; 225/3; 294/3; 382/3; 411/2; 448/3; 503/2  
C:Superfamily: protein kinase homology  
C:Keywords: ATP; phosphotransferase; protein kinase  
F:69-339/Domain: protein kinase homology <KIN>  
F:77-85/Region: protein kinase ATP-binding motif

Query Match	32.6%;	Score 847;	DB 2;	Length 557;
Best Local Similarity	44.3%;	Pred. No. 4.7e-31;		
Matches	171;	Conservative	75;	Mismatches 130;
				Indels 10;
				Gaps 5
Qy	46	LSREGILDALFVLPRECSQPALMKIKHVSFVRKYSDTIAELOELOPSAKDPEVRSLVCC	105	
Db	20	LGLEPLDULLGVHGLGASHLAQKVKVADFLQWVPIAARLKEVLQRDDFEILKVGIR	79	
Qy	106	GHFAEVQVVRKATGDIIYAMVKMKKALLACEQVSPFEERNILSRSTSPWTPQLQYAPQ	165	
Db	80	GAFSEVAVVMKQTSQVYAMKIMNKWDMLKGEVSCFREERDVLVKGDRRWITQLHFAFQ	139	
Qy	166	DKNHLYLWMEYOPGGDLSILNRRVEDQLDENLTFQVLAELIHAVSHLVGVVHRDIRPE	225	
Db	140	DENLYLWMEYVVGDDLTLLSKGERIPAMARFYLAEIVMAIDSVHRLGVYVHRDIRPD	199	
Qy	226	NILVDRTGHIKLIVFGSAAKMSNKWYNAKLPIGTDPDYVAPEVL-TVMNGDGKGTVGLDC	284	
Db	200	NILLDRCGHIRLADFGSCLKLPQGMVRSIVAVGTPDYLSPETLQAVGGPAGSGYGPEC	259	
Qy	285	DWMSGVGTAYEMIVGRSPFAGGTSGARTFNNIMNFQRLKPP-DDPKVSSDFLDLIQSLLC	343	
Db	260	DWALGVFAYEMFYGQTPFADSTAEYAKIVHYREHLSLPLADTVVPEEAQDLIRGLLC	319	
Qy	344	GOKERLKEG--LCCHPTFSKIDWNIRNSPPFPVPT-KSDDDSNFD--FPEKNSMVS	398	
Db	320	PAEIELRGGGAGDQKHPFFGLDWEGLRDSVPFPDPFEGATDTCNFVDVEDRLTAMVS	379	
Qy	399	SSPCCOLSPSGFS---GBELPFVGFYSY	421	
Db	380	GGGETLSDMQEDMPLGVRLPFVGSY	405	

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RESULT 11
G86431
protein kinase TS18.9 protein - Arabidopsis thaliana
C:Species:Arabidopsis thaliana (mouse-ear cress)
C:date: 02-Mar-2001 #sequence_revision 03-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86431

```

R.; Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huijzar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: G86431  
A:Status: preliminary  
A:Molecule type: DNA

[illegible]

QY	4	KRYGARNP--LDAGAAEPIANRASLNLFQGGPKPFMTQQCQWSPLSRSGILDALFVLPFE	61
Dd		: :	
Dd	265	YMYFPERRDOLLTKGTQDXAAVKLKIENFYQSSVKYAIERNNRRVELETEITSNWSSEER	324
QY	62	CSQPALKMKIKHVSNFVRKYSDTIALQLBELQPSAKDFEVRSILVGCGHFPAEVQVREKATGD	121
Dd		: :	
Dd	325	KSRQLSSIGLKESQFLR-----LRRLISLEDFHTVKVIGKGAFGEVRLVQKKDTGK	376
QY	122	IYAMVMKKKALLAQEQSVSFEEERNILSRSTPMIPOLQYAFODQNHLVLVMEVQSGGD	181
Dd		: :	
Dd	377	IYAMKTLKSEMYKDDQLAHVAERDVLAGSDSPWVSLYYSFQDAQLYLIMBFLPGGD	436
QY	182	LLSLNRVEDQDENLIQYLAELILAVSHLMGYVHRDIKPENILVDRTGHIKLYDFG	241
Dd		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Dd	437	LMTWLIRWQ-LFTEDVTFRVNAECILAETIHKLGFIHRDIKPNILIDIRGHIKLSDFG	495
QY	242	-----SAAKMSN-----	249
Dd		: :	
Dd	496	LSTGFPHKTHDSNYKKLLQQDEATNGISKPTYNANTTTANKQTWMVPDISLTMSNRQ	555
QY	250	-----KMVNKLPIGTDPDYMAPEVLTVNMGDGKGTGYGLDCDWWSVGVIAYEMIXGRS	301
Dd		: :	
Dd	556	QIQTWKRSMRLMAYSTVGTPTYIAPEIFYQG-----YGQECDWMSLGAIMECLIGWP	609
QY	302	PFAETSARTENNINMQREFLKFPDDPKVSSDFDLIQSLCCGOKERLKPEG-----LCCH	357
Dd		: :	
Dd	610	PFCEITPOETTRKMNVEQTLOFPDDLIHSYEADLIRLLTHADQRGLRGGADEIKSH	669
QY	358	PFFSKIDWNINRNPPFPVFPLTKDDDTSNFDEPKNSWVSSSPC-----QLSPSG	408
Dd		: :	
Dd	670	PFRFGVDWNTIROQEAEPVKLSIITDRTPPTDELEN-VPDSPAMAQAARQEOMTKQG	728
QY	409	FSG---HELPEVGFYSYK 423	
Dd		: :	
Dd	729	GSAPVKGDLPPIGYTSR 746	
RESULT 14			
S49077			
protein kinase PCTL7 (EC 2.7.1.-) - common tobacco			
C/Species: Nicotiana tabacum (common tobacco)			
C/Date: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004			
C/Acession: S49077			
R/Huang, Y.; Wan, J.; Ko, K.; Dennis, D.T.			
A/Submitted to the EMBL Data Library, December 1992			
A/Description: A CAMP-dependent protein kinase homolog in tobacco leaf.			
A/Reference number: S49077			
A/Acession: S49077			
A/Molecule type: mRNA			
A/Residues: 1-526 <HUA>			
A/Cross-references: UNIPROT:Q40547; EMBL:X71057; NID:G506533; PID:NCAA50374.1; PID:G5065			
C/Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology			
C/Keywords: Atg; phosphotransferase; protein kinase			
F/109-420/Domain: protein kinase homology <KIN>			
F/117-125/Region: protein kinase ATP-binding motif			
Query Match			
Best Local Similarity 35.9%; Pred. No. 1.4e-24;			
Matches 160; Conservative 74; Mismatches 144; Indels 68; Gaps 8;			
QY	76	FVRKYSDTIALQLQPSAKDFEVRSILVGCGHFAEV-----QVVRKATGIIVA	124
Dd		: :	
Dd	90	FLEKETERYMLRQHKNMGADDPELLTMIGKAEGEPICMIGFSVITGONCREKTTGGVYA	149
QY	125	KMYMKKALLAQBQSVSFEEERNILSRSTPMIPOLQYAFODQNHLVLVMEVQSGDLLS	184
Dd		: :	
Dd	150	MKKLKKSEMLRRQGVHVHVAERNLLAEVSDCIKLVYSFQDDDYLLVWEVLPQGDMMT	209
QY	185	LLNRYEDQDENLIQYLAELILAVSHLMGVVHRDIKPENILVDRTGHIKLYDFGSAA	244
Dd		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Dd	210	LUMR-KDILTDEARFYVAETVLAISSIHKNYIHRDIKPDNLILLDRYGHKLKSIFGLCK	268

QY 245 KNN-----SNKQVNAKLPIGTPDYNA 265  
 Db 269 PLDCSTLBEKFSVDNANGSRSDPPAPKRTQOELEHWQNRRLAYSTVGTPDYIA 328  
 QY 266 PEVLTVNMGDGKGTGYGLDGDWMSGVIAIYEMLYGRSPFAEGTSARTFNINNFQFLKFP 325  
 Db 329 PEVLV-----KKGYGMECDNWSLGAINYEMLVGPPFYSDPMSTCRKIWNKHLKFP 382  
 QY 326 DDPKVSDFLDIOLSLGCGKERLKFEQ---LCCHPPFSKIDMNNIRNSPPFPVPTLKSD 382  
 Db 383 EEAKLSPKAIISRLLCNVTERLCSNGADEIKVHSWPKGIDWDRIYQMEAAFIPEVND 442  
 QY 383 DDTSNFDEPEKNSWSSPQCLSP--SGFSCEELPFYGFYSKALGILGRSESIVSGLDS 440  
 Db 443 LDTQNFKEFESESHSGSGSRGFWRKWLSKQDNFVGITYYKNPKV---NDYQVPGMVE 499  
 QY 441 PAKTSSMEKLLIKS---KELQDSQD 463  
 Db 500 LKTNTPKPKPTIKSLFGDESEASED 525

RESULT 15  
 T41723  
 serine/threonine-specific protein kinase (EC 2.7.1.-) orb6 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
 C:Accession: T41723; T43526  
 R:Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, October 1999  
 A:Reference number: Z22012  
 A:Accession: T41723  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-469 <RIE>  
 A:Cross-references: UNIPROT:O13310; EMBL:AL121770; PIDN:CBAS7446.1; GSPDB:GN00066; SPDB:SPDB0000066  
 A:Experimental source: strain 972H-; cosmid c821  
 R:Verde, F.; Wiley, D.J.; Nurse, P.  
 Proc. Natl. Acad. Sci. U.S.A. 95, 7526-7531, 1998  
 A:Title: Fission yeast orb6, a ser/thr protein kinase related to mammalian rho kinase at the cell cycle.  
 A:Reference number: Z22544; MUID:98301608; PMID:9636183  
 A:Accession: T43526  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-469 <VER>  
 A:Cross-references: EMBL:AF095912; NID:G2443510; PIDN:AAC32420.1; PID:G2443511  
 C:Genetics:  
 A:Gene: orb6; SPAC821.12  
 A:Map position: 1  
 A:Introns: 48/2; 106/3  
 C:Function:  
 A:Description: coordinates maintenance of cell polarity during interphase with the onset of mitosis  
 A:Note: interacts genetically with orb2, which encodes the Pak1/Shk1 protein kinase  
 C:Superfamily: protein kinase homology  
 C:Keywords: phosphotransferase

Query Match 26.9%; Score 700; DB 2; Length 469;  
 Best Local Similarity 39.2%; Pred. No. 1.4e-24;  
 Matches 148; Conservative 63; Mismatches 113; Indels 54; Gaps 8;

QY 93 SAKDFEVRSLVGGCHFAEYQVVRKATGDIYAMKWKKKALLAQEOVSFEFERNTLSRS 152  
 Db 89 SLEDFSTIKVIGKGAAGEVRLVQKLDITGKIYANKSLKTEMFKDQLAHVKAERDLULVES 148  
 QY 153 TSPWIPQLOYAQDKNHLYLVNVEYQPGDLLSLNRYEDQDLNLTQFYLAELILAVHSV 212  
 Db 149 DSGPVVWSLYAFQDSLYLYLIMEFLPGGSLMTWLINY-DTFSEDVTRFYVAECVLAIDV 207  
 QY 213 HLMGVYVHRDIKPENTILVDRTHGILKLVDFG-----SAAKM----- 246  
 Db 208 HRNGYIHRDIKPENTILIDRDGHILKSLDGLSTGFYKQDOSASYNMKPRTGNTVKRGQVDA 267  
 QY 247 -----NSNKMNNAKLPIGTPDYNAPEVLTVNMGDGKGTGYGLDGDWMSGVYI 292

Fri Nov 12 12:26:07 2004

Db	268	IWLTSSKDKMATWKNRRVWYSTVGTDPDYIAPEIF-LQOG-----YQDCDWWSLGAI	321
Qy	293	AYEMMYGRSFFAEGTSARTFNINMNFQRLKFPDDPKVSSDFDLIOSLLCQOKERLXFE	352
Db	322	MPECLIGWPPFCSENSHETYRKIIINWRETITFPNDIHLSIEARDLMDRLMTDSEHRLGRG	381
Qy	353	G---LCCHPFFSKIDWNIRNSPPFPVPTLKSDDDTSNF--DEPEK--NSWYSSSPCOLS	405
Db	382	GAIEIMQHFFFTGIDWDHIRETAAPFIPNLKSIITDTHYFPVDELEQVPEQPVTQOPASVD	441
Qy	406	PSGFSGEELPFVGFYSYK	423
Db	442	PQLEQTNLAFGLGYTKK	459

Search completed: November 8, 2004, 12:32:19  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 12:18:30 ; Search time 156 Seconds  
(without alignments)  
1142.875 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKFKYGARPLDAGAEPI.....CSRILPSVYAKGARGCWL 497

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	497	6	ABU10126
2	2602	100.0	497	7	Aae39504
3	2602	100.0	497	8	ADO40592
4	2597	99.8	497	6	ABP97687
5	2589	99.5	497	5	Aae16261
6	2589	99.5	497	6	ABU10127
7	2582	99.2	495	6	ABP97681
8	2440	93.8	620	6	ADN62809
9	2440	93.8	623	6	ADA05644
10	2440	93.8	1958	5	ABB81928
11	2440	93.8	2054	5	ABB81927
12	2440	93.8	2054	5	Aae24150
13	2440	93.8	2054	6	AAO26959
14	2430	93.4	2053	7	Aae24079
15	2430	93.4	2053	7	ADP60994
16	2418.5	92.9	2053	4	AAU03501
17	2418.5	92.9	2053	8	ADJ96610
18	2412.5	92.7	2053	5	ABG78363
19	2412.5	92.7	2053	6	ADA05642
20	2412.5	92.7	2053	8	ADN63228
21	2412.5	92.7	2053	8	ADN62807
22	2412.5	92.7	2066	6	ABG78362
23	2412.5	92.7	2066	5	ADA05654
24	2400.5	92.3	2066	8	ADN62819
25	2271.5	87.3	494	6	ABP97682

26	2271.5	87.3	494	8	ADO40594
27	2172.5	83.5	2055	6	ABP97683
28	2172.5	83.5	2055	6	AAO26980
29	1652	63.5	319	7	ADN62730
30	1627	62.5	349	4	ABG15566
31	1284	49.3	257	7	ADJ79947
32	1180	45.3	251	7	ADJ79949
33	1177	45.2	251	7	ADJ79950
34	932.5	35.8	1565	8	ADP47967
35	929	35.7	475	5	AAE24131
36	929	35.7	1197	6	ABJ37881
37	929	35.7	1247	6	ABJ37882
38	929	35.7	1551	8	ADJ40850
39	929	35.7	1553	7	ADG99064
40	929	35.7	1569	8	ADP95102
41	929	35.7	1572	5	AAE19162
42	929	35.7	1572	8	ADJ96611
43	926	35.6	1548	8	ADP95100
44	922	35.4	1252	4	ABB66357
45	896.5	34.5	1000	7	ADB82759

## ALIGNMENTS

RESULT 1  
ABU10126  
ID ABU10126 standard; protein; 497 AA.  
XX  
AC ABU10126;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Novel human kinase.  
XX  
KW Human; enzyme; gene therapy; kinase; antisense.  
XX  
OS Homo sapiens.  
XX  
PN US2003022340-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 11-SEP-2002; 2002US-00238709.  
XX  
PR 13-MAR-2001; 2001US-00804471.  
XX  
(APPL-) APPLERA CORP.  
XX  
Webster M, Yan C, Di Francesco V, Beasley EM;  
WPI: 2003-439978/41.  
N-P9DB; ACA61394.  
New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.  
Claim 1; Fig 2; 207pp; English.  
The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the corresponding biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for



CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or in treatment  
 CC regimen, in gene therapy and as antisense constructs to control  
 CC transporter gene expression in cells, tissue and organisms. The present  
 CC sequence represents the amino acid sequence of a novel human kinase  
 XX  
 SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 6; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAPIANRSLNLFQGGKPPMTQOQSPISREGILDALVLFEE 60  
 Db 1 MLKFKYGARNPLDAGAAPIANRSLNLFQGGKPPMTQOQSPISREGILDALVLFEE 60  
 QY 61 ECSQPALMKIKHVSFNFKYSDTIAELQELQPSAKDFEVSRLVGGCGHFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFNFKYSDTIAELQELQPSAKDFEVSRLVGGCGHFAEVQVREKATG 120  
 QY 121 DIYAMKVMKKALLAQEQVSFEERNILGRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 Db 121 DIYAMKVMKKALLAQEQVSFEERNILGRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEQDENLIQFYLAELIIVAVSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEQDENLIQFYLAELIIVAVSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
 QY 241 GSAAKMNSKVMNAKPLIGTDPYNAPEVLVWNGDGKGTGLDCDWSGVIAEYMIYGR 300  
 Db 241 GSAAKMNSKVMNAKPLIGTDPYNAPEVLVWNGDGKGTGLDCDWSGVIAEYMIYGR 300  
 QY 301 SPFAEGTSARTFNIMAFQRLKFPDPPKVSDFDLIQSLCGQKRLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNIMAFQRLKFPDPPKVSDFDLIQSLCGQKRLKFEGLCCHPFF 360  
 QY 361 SKIDWNNIRNSPPFPVPTLKSDDTNSFDEPEKNSVSSPCQLSPGSGBELPVGFS 420  
 Db 361 SKIDWNNIRNSPPFPVPTLKSDDTNSFDEPEKNSVSSPCQLSPGSGBELPVGFS 420  
 QY 421 YSKALGILGRESVVGSLDPAKTSMEKLLIKSELQDSQDKCHKVIFISAAGLLPCSR 480  
 Db 421 YSKALGILGRESVVGSLDPAKTSMEKLLIKSELQDSQDKCHKVIFISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 2  
 AAE39504  
 ID AAE39504 standard; protein; 497 AA.  
 AC AAE39504;  
 DT 18-DEC-2003 (first entry)  
 DE Human kinase protein.  
 KW Human; kinase protein; diagnostic; therapeutic; immune response; enzyme;  
 KW pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 50..55  
 FT /note= "N-myristoylation site"  
 FT Modified-site 78..81  
 FT /note= "cAMP and cGMP dependent protein kinase  
 phosphorylation site"  
 FT Modified-site 83..86  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 93..96

FT Modified-site  
 FT 93..95  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Region 103..126  
 FT /note= "Protein kinase Atp-binding region signature"  
 FT Modified-site 140..143  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Region 197..217  
 FT /note= "Helix I"  
 FT Active-site 217..229  
 FT /note= "Serine/Threonine protein kinase active-site  
 signature"  
 FT Modified-site 248..250  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 308..310  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 361..364  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Misc-difference 365  
 FT /note= "This residue changes to Cys during single  
 nucleotide polymorphism (SNP)"  
 FT Modified-site 378..380  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 381..384  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 386..389  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 410..413  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 436..439  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 445..448  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Region 467..487  
 FT /note= "Helix II"  
 FT Modified-site 474..479  
 FT /note= "N-myristoylation site"  
 FT Modified-site 489..494  
 FT /note= "N-myristoylation site"  
 FT Modified-site 490..492  
 FT /note= "Protein kinase C phosphorylation site"  
 FN US2002132322-A1.  
 PD 19-SEP-2002.  
 DP 13-MAR-2001; 2001US-00804471.  
 XX 13-MAR-2001; 2001US-00804471.  
 PA (WEBS/) WEBSTER M.  
 PA (YANC/) YAN C.  
 PA (DPRA/) DI FRANCESCO V.  
 PA (BEAS/) BEASLEY E M.  
 XX Webster M, Yan C, Di Francesco V, Beasley EM;  
 DR WPI; 2003-687480/65.  
 DR N-PSDB; AAD59937, AAD59938.  
 XX New isolated human kinase proteins, useful as models for developing human  
 PT therapeutic targets, or for treating a disorder associated with an  
 PT absence of, inappropriate or unwanted expression of the protein, e.g.  
 FT cancer.  
 FT Claim 1; Fig 2; Opp; English.  
 XX The present invention relates to human kinase proteins and nucleic acids  
 CC encoding them all of which are useful in the development of human  
 CC therapeutics and diagnostic composition and methods. The invention is  
 CC useful as models for the development of human therapeutic targets, aid in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents. The invention is also useful in



CC drug screening assays, in assays to determine the biological activity of  
 CC the protein, to raise antibodies and to elicit another immune response.  
 CC The antibodies are useful in pharmacogenomic analysis, for inhibiting  
 CC protein function and for tissue typing. The transgenic animals are useful  
 CC for studying the function of kinase protein, identifying and evaluating  
 CC modulators of kinase protein activity. The invention is also used in gene  
 CC therapy. The present sequence is the human kinase protein. The human  
 CC kinase gene is located on chromosome 12  
 XX

SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 7; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARPLDAGAEPTANRASRLNLFQGGPPPTQOQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARPLDAGAEPTANRASRLNLFQGGPPPTQOQMSPLSREGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

QY 121 DIYAMKMKKALLAQGVQSFPEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180  
 Db 121 DIYAMKMKKALLAQGVQSFPEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180

QY 181 DLASLLNRYEDQDENLIQYLAELILAVHSVHLMGVVHRDIKPNILVDRTHIKLVDF 240  
 Db 181 DLASLLNRYEDQDENLIQYLAELILAVHSVHLMGVVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKMNSNRQVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSGVIAEYMIYGR 300  
 Db 241 GSAAKMNSNRQVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSGVIAEYMIYGR 300

QY 301 SPFAEGTSARTENNINNFQFLKPDPPKVSDFDLIQLSLCGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTENNINNFQFLKPDPPKVSDFDLIQLSLCGQKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSVSSPCQLSPSGFSGBELPVGFS 420  
 Db 361 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSVSSPCQLSPSGFSGBELPVGFS 420

QY 421 YSKALGILGSESVWSGLSPAKTSSMEKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480  
 Db 421 YSKALGILGSESVWSGLSPAKTSSMEKLLIKSKELQSDQKCHKVFIISAAGLLPCSR 480

QY 481 ILPSVYAKGSARGCWL 497  
 Db 481 ILPSVYAKGSARGCWL 497

RESULT 3

ADO40592  
 ID ADO40592 standard; protein; 497 AA.

XX AC ADO40592;

XX DT 29-JUL-2004 (first entry)

XX DE Human kinase protein.

XX KW Kinase; rho/rac-interacting citron kinase; drug screening;

XX KW kinase related disorder; human; enzyme.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 50..55

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 78..81

FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"

FT

FT Modified-site 83..86  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 93..96  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 93..95  
 FT /note= "protein kinase C phosphorylation site"  
 FT Binding-site 103..126  
 FT /note= "protein kinase ATP-binding region signature"  
 FT Modified-site 140..143  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Region 197..217  
 FT /note= "Helix 1"  
 FT Active-site 217..229  
 FT /note= "Serine/Threonine protein kinase active-site signature"  
 FT Modified-site 248..250  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 308..310  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 361..364  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 378..380  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 381..384  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 386..389  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 410..413  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 436..439  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 445..448  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Region 467..487  
 FT /note= "Helix 2"  
 FT Modified-site 474..479  
 FT /note= "N-myristoylation site"  
 FT Modified-site 489..494  
 FT /note= "N-myristoylation site"  
 FT Modified-site 490..492  
 FT /note= "Protein kinase C phosphorylation site"

US2004091993-A1.

13-MAY-2004.

02-DEC-2003; 2003US-00724594.

13-MAR-2001; 2001US-00804471.

11-SEP-2002; 2002US-00238709.

(APPL-) APPLERA CORP.

Webster M, Yan C, Di Francesco V, Beasley EM;

WPI; 2004-374957/35.

N-ESDB; ADO40591, ADO40593.

New isolated human kinase proteins and nucleic acids, useful for developing human therapeutic targets, identifying therapeutic proteins or serve as targets for the development of human therapeutic agents that modulate kinase activity.

Claim 1; SEQ ID NO 2; 207pp; English.

The present invention provides a kinase polypeptide and its encoding polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, and in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and

CC unwanted expression of the protein. The present sequence is the human  
 CC kinase protein.  
 XX  
 XX Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 8; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLE 60  
 DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLE 60  
 QY 61 ECSQALMKIKHVSNFVRKYSDTIABLOQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 DB 61 ECSQALMKIKHVSNFVRKYSDTIABLOQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 QY 121 DIYAMKMKKALLAQEQVSFEEERNILSRSTSPWIPQLQYAFQDKNHLVMEYQPGG 180  
 DB 121 DIYAMKMKKALLAQEQVSFEEERNILSRSTSPWIPQLQYAFQDKNHLVMEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDKPENILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDKPENILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 DB 241 GSAAKNSNMKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 QY 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSDFDLILQSLCGQKRLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSDFDLILQSLCGQKRLKFEGLCCHPFF 360  
 QY 361 SKIDWNINRSPFPVPTLKSDDDTSNFDEPEKNSWSSPCOLSPSGSGEELPFVGF 420  
 DB 361 SKIDWNINRSPFPVPTLKSDDDTSNFDEPEKNSWSSPCOLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFI SAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFI SAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 DB 481 ILPSVYAKSGARGCWL 497

RESULT 4  
 ID ABP97687 standard; protein; 497 AA.  
 AC ABP97687;  
 XX  
 XX  
 XX 16-MAY-2003 (first entry)  
 XX  
 XX Amino acid sequence of citron rho/rac-interacting kinase-short kinase.  
 DE Human; citron rho/rac-interacting kinase-short kinase; obesity;  
 DE chronic obstructive pulmonary disease; hypertension; diabetes;  
 DE coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
 DE gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
 DE polycystic ovarian syndrome; fertility; depression.  
 XX Homo sapiens.  
 OS  
 XX  
 XX W02003004629-A2.  
 XX  
 XX 16-JAN-2003.  
 XX  
 XX 01-JUL-2002; 2002WO-EP007229.  
 XX  
 XX 02-JUL-2001; 2001US-0301853P.  
 PR 10-DEC-2001; 2001US-0337130P.  
 PR 25-APR-2002; 2002US-0375015P.

(FARB ) BAYER AG.  
 Zhu 2;  
 WPI; 2003-221595/21.  
 N-PSDB; AB268726.  
 New human citron rho/rac-interacting kinase-short kinase polypeptide and polynucleotide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary disease.  
 Claim 1; Fig 19; 145pp; English.  
 The present sequence represents a human citron rho/rac-interacting kinase -short kinase polypeptide. The polynucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced fertility, and depression  
 Sequence 497 AA;

Query Match 99.8%; Score 2597; DB 6; Length 497;  
 Best Local Similarity 99.8%; Pred. No. 6.5e-254;  
 Matches 496; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLE 60  
 DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLE 60  
 QY 61 ECSQALMKIKHVSNFVRKYSDTIABLOQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 DB 61 ECSQALMKIKHVSNFVRKYSDTIABLOQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 QY 121 DIYAMKMKKALLAQEQVSFEEERNILSRSTSPWIPQLQYAFQDKNHLVMEYQPGG 180  
 DB 121 DIYAMKMKKALLAQEQVSFEEERNILSRSTSPWIPQLQYAFQDKNHLVMEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDKPENILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDKPENILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 DB 241 GSAAKNSNMKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 QY 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSDFDLILQSLCGQKRLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSDFDLILQSLCGQKRLKFEGLCCHPFF 360  
 QY 361 SKIDWNINRSPFPVPTLKSDDDTSNFDEPEKNSWSSPCOLSPSGSGEELPFVGF 420  
 DB 361 SKIDWNINRSPFPVPTLKSDDDTSNFDEPEKNSWSSPCOLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFI SAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFI SAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 DB 481 ILPSVYAKSGARGCWL 497

RESULT 5  
 AAEL6261

AD	AAE16261	standard; protein; 497 AA.
XX	AC	AAE16261;
XX	XX	
DT	26-MAR-2002	(first entry)
XX	XX	
DE	Human kinase PKIN-7 protein.	
XX	Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;	
XX	immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;	
KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;	
KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;	
KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;	
KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;	
KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;	
KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;	
KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;	
KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;	
KW	fatty liver; Niemann-Pick's disease; gene therapy.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FT	Domain	86..124
FT	Domain	/label= Protein_kinase_domain
FT	Domain	96..153
FT	Domain	/label= Protein_kinase_domain
FT	Domain	97..360
FT	Domain	/note= "Eukaryotic protein kinase domain"
FT	Domain	98..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	99..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	101..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	102..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	249..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	258..445
FT	Domain	/label= Protein_kinase_domain
FT	Domain	258..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	361..390
FT	Domain	/note= "Protein kinase C terminal domain"
XX	WO200196547-A2.	
XX	20-DEC-2001.	
XX	14-JUN-2001;	2001WO-US019444.
XX	15-JUN-2000;	2000US-0212073P.
PR	23-JUN-2000;	2000US-0213467P.
PR	30-JUN-2000;	2000US-0215651P.
PR	07-JUL-2000;	2000US-0216059P.
PR	13-JUL-2000;	2000US-0218372P.
PR	25-AUG-2000;	2000US-0228056P.
XX	(INCY-)	INCYTE GENOMICS INC.
XX	Yue H, Lal P, Bandnan O, Borowsky ML, Au-Young J, Lu Y;	
PI	Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DAM, Greenwald SR;	
PI	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;	
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;	
PI	Lo TP, Khan F, Recipon SA, Azinzai Y, Policky JL, Ding L;	
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;	
XX	WPI: 2002-090207/12.	
DR	N-PSDB; AAD26454.	
XX		
PT	New polypeptides, useful for diagnosing, treating or preventing disorders	
PT	of growth and development, cardiovascular and lipid, and diseases such as	
PT	cancer, comprise human kinase polypeptides.	
XX	Claim 1; Page 146-147; 197pp; English.	
XX	The invention relates to human kinase PKIN proteins and their	
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for	
CC	treating a disease or condition associated with decreased expression of	
CC	PKIN and a composition comprising PKIN antagonist is useful for treating	
CC	a disease or condition associated with overexpression of PKIN. The	
CC	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,	
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder	
CC	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,	
CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,	
CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes	
CC	mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,	
CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,	
CC	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,	
CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections	
CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,	
CC	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio	
CC	vascular disease (arteriovenous fistula, hypertension, vasculitis,	
CC	aneurysms, congestive heart failure, angina pectoris, myocarditis,	
CC	ischaemic heart disease, chronic bronchitis, lung tumours); lipid	
CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,	
CC	hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity	
CC	of a test compound and in gene therapy. The present sequence is human	
CC	PKIN-7 protein	
XX		
SQ	Sequence 497 AA;	
XX		
XX	Query Match	99.5%; Score 2589; DB 5; Length 497;
XX	Best Local Similarity	99.6%; Pred. No. 4.2e-253;
XX	Matches	495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1	MLKFKYGARNPLDAGAAEPTANRSLNLFPGQFPPTQOQMSPLREGILDALFVLF 60
DB	1	MLKFKYGARNPLDAGAAEPTANRSLNLFPGQFPPTQOQMSPLREGILDALFVLF 60
QY	61	ECSPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVREKATG 120
DB	61	ECSPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVREKATG 120
QY	121	DIYAMKVKKKALLAQEQVFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLYMEYOPGG 180
DB	121	DIYAMKVKKKALLAQEQVFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLYMEYOPGG 180
QY	181	DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240
DB	181	DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240
QY	241	GSAAKNSNKNVNAKLPIGTDPYMAPEVLTVANGDGKTYGLDCDMSVGVIAVEMYGR 300
DB	241	GSAAKNSNKNVNAKLPIGTDPYMAPEVLTVANGDGKTYGLDCDMSVGVIAVEMYGR 300
QY	301	SPPAEGTSARTFNINMFORFLKPPDDPKVSSDFLDLIQSLLCGKERLKEGLCCHPFF 360
DB	301	SPPAEGTSARTFNINMFORFLKPPDDPKVSSDFLDLIQSLLCGKERLKEGLCCHPFF 360
QY	361	SKIDMNNIRNSPPFPVPTLTKSDDDTNFDPEFNKSNVSSSPCQLSPSGFSGEELPFVGF 420
DB	361	SKIDMNNIRNSPPFPVPTLTKSDDDTNFDPEFNKSNVSSSPCQLSPSGFSGEELPFVGF 420
QY	421	YSKALGILGHSESVSGLOSPAKTSSMEKLLIKSKELQDSQDKCHKVFIISAGLLPCSR 480
DB	421	YSKALGILGHSESVSGLOSPAKTSSMEKLLIKSKELQDSQDKCHKVFIISAGLLPCSR 480
QY	481	ILPSVYAKGSARGCWL 497
DB	481	ILPSVYAKGSARGCWL 497
XX	RESULT 6	
XX	ABU10127	

ID XX ABU10127 standard; protein; 497 AA.  
XX AC ABU10127;  
XX DT 11-AUG-2003 (first entry)  
XX DE Variant novel human kinase.  
XX KW Human; enzyme; gene therapy; kinase; antisense.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 365  
XX FT /note= "Wild-type Trp substituted by Cys as a result of a  
XX FT single nucleotide polymorphism"  
XX PN US2003022340-A1.  
XX PD 30-JAN-2003.  
XX PF 11-SEP-2002; 2002US-00238709.  
XX PR 13-MAR-2001; 2001US-00804471.  
XX PA (APPL-) APPLERA CORP.  
XX PI Webster M, Yan C, Di Francesco V, Beasley EM;  
XX WIPI; 2003-438978/41.  
XX New human kinase peptides useful as models or targets for the development  
XX of therapeutic agents that modulate kinase activity, for eliciting immune  
XX response, and in identifying compounds that modulate kinase activity or  
XX expression.  
XX Disclosure; Page; 207pp; English.  
XX The invention relates to a novel isolated human kinase. The kinase  
XX peptides and nucleic acids are useful as models for the development of  
XX human therapeutic targets, in the identification of therapeutic proteins,  
XX and serve as targets for the development of human therapeutic agents that  
XX modulate kinase activity in cells and tissues that express the kinase.  
XX The proteins can be used to raise or to elicit another immune response.  
XX as a reagent in assays designed to determine the levels of the protein in  
XX biological fluids, as markers for tissue in which the corresponding  
XX protein is preferentially expressed, in the identification of modulators  
XX of the peptides and in pharmacogenomic analysis. The nucleic acids are  
XX useful as hybridisation probes, in constructing vectors, host cells or  
XX transgenic animals expressing all or a part of the nucleic acid, for  
XX monitoring the effectiveness of modulating compounds on the expression or  
XX activity of the transporter gene in clinical trials or in treatment  
XX regimen, in gene therapy and as antisense constructs to control  
XX transporter gene expression in cells, tissue and organisms. The present  
XX sequence represents the amino acid sequence of a variant novel human  
XX kinase. Note: The present sequence is not shown in the specification but  
XX was created by the indexer using the information given in figure 3  
XX  
XX Sequence 497 AA;  
Query Match 99.5%; Score 2589; DB 6; Length 497;  
Best Local Similarity 99.8%; Pred. NO. 4.2e-253;  
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKFYKGNPLDAGAEPTANRSLNLFQCKPPEMTQQQMSPLSREGILDALFVLFE 60  
DB 1 MLKFYKGNPLDAGAEPTANRSLNLFQCKPPEMTQQQMSPLSREGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180

DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
QY 241 GSAAXKNSNMYNAKLPIGTPDYMAPEVLTVNMGCKGTGGLDCDMSVGVYAYEMIKGR 300  
DB 241 GSAAXKNSNMYNAKLPIGTPDYMAPEVLTVNMGCKGTGGLDCDMSVGVYAYEMIKGR 300  
QY 301 SPFAECTSARTFNINMFORFLKFPDDPKVSSDFDLIQLSLCGQKRLKFEGLCCHPFF 360  
DB 301 SPFAECTSARTFNINMFORFLKFPDDPKVSSDFDLIQLSLCGQKRLKFEGLCCHPFF 360  
QY 361 SKIDMNINSPPPVFTLKSDDDTSNFDPEPKNSWSSPCQLSPSGFSGEELPFVGF 420  
DB 361 SKIDCNIRNSPPFPVFTLKSDDDTSNFDPEPKNSWSSPCQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKVIFISAAGLLPCSR 480  
DB 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKVIFISAAGLLPCSR 480  
QY 481 ILPSVYAKGSARGCWL 497  
DB 481 ILPSVYAKGSARGCWL 497  
RESULT 7  
ABP97681  
ID ABP97681 standard; protein; 495 AA.  
XX AC ABP97681;  
XX DT 16-MAY-2003 (first entry)  
XX DE Amino acid sequence of citron rho/rac-interacting kinase-short kinase.  
XX KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
XX chronic obstructive pulmonary disease; hypertension; diabetes;  
XX coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
XX gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
XX polycystic ovarian syndrome; fertility; depression.  
XX OS Homo sapiens.  
XX WO2003004629-A2.  
XX 16-JAN-2003.  
XX 01-JUL-2002; 2002WO-EP007229.  
XX 02-JUL-2001; 2001US-0301853P.  
XX 10-DEC-2001; 2001US-0337130P.  
XX 25-APR-2002; 2002US-0375015P.  
XX (FARB ) BAYER AG.  
XX Zhu Z;  
XX WIPI; 2003-221595/21.  
XX N-PSDB; ABZ68725.  
XX New human citron rho/rac-interacting kinase-short kinase polypeptide and  
XX polynucleotide for preventing or treating diseases associated with the  
XX polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
XX disease.  
XX Claim 1; Fig 2; 145pp; English.  
XX The present sequence represents a human citron rho/rac-interacting kinase  
XX -short kinase polypeptide. The polynucleotide and polypeptide of the  
XX invention are useful in preventing, ameliorating, or treating diseases

CC associated with the polypeptide dysfunction. The expression vector or the  
CC reagent is useful in the preparation of a medicament for modulating the  
CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
CC disease, such as obesity or chronic obstructive pulmonary disease. These  
CC may also be used for treating obesity/ overweight-associated  
CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
CC fertility, and depression  
XX  
SQ Sequence 495 AA;

Query Match 99.2%; Score 2582; DB 6; Length 495;  
Best Local Similarity 99.8%; Pred. No. 2.2e-252;  
Matches 494; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNFLDAGAEPIANRASRLNLFQGGPPFMTQQMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNFLDAGAEPIANRASRLNLFQGGPPFMTQQMSPLSREGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSNFVKYSDTTAELOELOPSAKOFEVRSVLCGCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSNFVKYSDTTAELOELOPSAKOFEVRSVLCGCHFAEVQVREKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180  
DB 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180  
QY 181 DLLSLNRYEOLDENLIQFYLAELILAVHSVHLMGVVHRDIPENILVDRTHGKLVDF 240  
DB 181 DLLSLNRYEOLDENLIQFYLAELILAVHSVHLMGVVHRDIPENILVDRTHGKLVDF 240  
QY 241 GSAAKNKNKVMNAKLPICTPDYMAPEVLTVMNGDGKGTGYGLDCDWMVSGVIAYEMIYGR 300  
DB 241 GSAAKNKNKVMNAKLPICTPDYMAPEVLTVMNGDGKGTGYGLDCDWMVSGVIAYEMIYGR 300  
QY 301 SPFAEGTGAFTNNIMNFORLKFDPDKYSSDPLDLIQSLCCQKRLKFEGLCCHPFF 360  
DB 301 SPFAEGTGAFTNNIMNFORLKFDPDKYSSDPLDLIQSLCCQKRLKFEGLCCHPFF 360  
QY 361 SKIDNNNRNPPPPVPTLKSDDDTSNFDPEKNSWSSPQOLSPGSGEELPFVGF 420  
DB 361 SKIDNNNRNPPPPVPTLKSDDDTSNFDPEKNSWSSPQOLSPGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
DB 421 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
QY 481 ILPSVYAKGSARGRC 495  
DB 481 ILPSVYAKGSARGRC 495

RESULT 8  
ADN62809  
ID ADN62809 standard; protein; 620 AA.

XX AC ADN62809;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV1b.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;  
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;  
wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

PD 26-FEB-2004.  
XX 01-OCT-2002; 2002US-00262511.  
XX 02-OCT-2001; 2001US-0326483P.  
PR 05-OCT-2001; 2001US-0327435P.  
PR 09-OCT-2001; 2001US-0327917P.  
PR 09-OCT-2001; 2001US-0328029P.  
PR 09-OCT-2001; 2001US-0328044P.  
PR 09-OCT-2001; 2001US-0328056P.  
PR 12-OCT-2001; 2001US-0328849P.  
PR 15-OCT-2001; 2001US-0329414P.  
PR 17-OCT-2001; 2001US-0330142P.  
PR 18-OCT-2001; 2001US-0330309P.  
PR 22-OCT-2001; 2001US-0341058P.  
PR 24-OCT-2001; 2001US-0339266P.  
PR 29-OCT-2001; 2001US-0343629P.  
PR 01-NOV-2001; 2001US-0349575P.  
PR 17-APR-2002; 2002US-0373260P.  
PR 19-APR-2002; 2002US-0373815P.  
PR 19-APR-2002; 2002US-0373817P.  
PR 19-APR-2002; 2002US-0373826P.  
PR 19-APR-2002; 2002US-0373884P.  
PR 22-APR-2002; 2002US-0374977P.  
PR 16-MAY-2002; 2002US-0381037P.  
PR 16-MAY-2002; 2002US-0381038P.  
PR 16-MAY-2002; 2002US-0381042P.  
PR 17-MAY-2002; 2002US-0381642P.  
PR 28-MAY-2002; 2002US-0383656P.  
PR 29-MAY-2002; 2002US-0383831P.  
PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J. A.  
PA (KEKO/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
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PA (PATT/) PATTURAJAN M.  
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PA (EDIN/) EDINGER S. R.  
PA (ELLE/) ELLERMAN K. R.  
PA (MALY/) MALYANKAR U. M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
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PA (ANDE/) ANDERSON D. W.  
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PA (PEN/) PENNA C. E. A.  
PA (SHEN/) SHENOY S. G.  
PA (SHIM/) SHIMKETS R. A.  
PA (ROTH/) ROTHENBERG M. E.  
PA (LEAC/) LEACH M. D.  
PA (AGEE/) AGEE M. L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPPIO V. A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E. A.  
PA (RIEG/) RIEGER D. K.  
PA (SPAD/) SPADERNA S. K.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
Patturajan M, Spytek KA, Ellerman K, Malyankar UM;  
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;  
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

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us-10-724-594-2.rag

PI Shimkets RA, Rotherberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;  
XX  
XX  
XX WPI: 2004-213931/20.  
DR N-PSDB; ADM62808.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.  
XX  
XX  
XX Claim 1; SEQ ID NO 4; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.  
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or  
CC treat a medical condition in human related to the aberrant expression and  
CC activity of NOVX polypeptides. For example, NOVX polypeptides and  
CC polynucleotides may be used to treat disorders associated with decreased  
CC expression or activity of NOVX by supplementing the patient our  
CC production or to rectify mutations. Conversely, antisense NA molecules  
CC may be administered to down regulate expression of NOVX polypeptides by  
CC binding with the cells own genes and preventing their expression. NOVX  
CC polynucleotides and complementary sequences may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar sequences in samples, and so which patients may be in need of  
CC restorative therapy. NOVX polypeptides may also be used as antigens in  
CC the production of antibodies and in assays to identify modulators  
CC (agonists and antagonists) of the expression and activity of NOVX. The  
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be  
CC used to modulate NOVX polynucleotide expression and activity of NOVX  
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as  
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX  
CC polypeptides and polynucleotides may be used in this way to prevent,  
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious  
CC diseases, anorexia, cancer, cancer-associated cachexia, neurodegenerative  
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. The present sequence  
CC represents the amino acid sequence of a human NOVX protein.

XX SQ Sequence 620 AA;

Query Match 93.8%; Score 2440; DB 8; Length 620;  
Best Local Similarity 99.6%; Pred. No. 8.1e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLREGIIDLALFVLFE 60  
DB 5 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLREGIIDLALFVLFE 64  
QY 61 ECSQPALMKIKHVSFNFRKYSYDIAELQELQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
DB 65 ECSQPALMKIKHVSFNFRKYSYDIAELQELQPSAKDFEVRSLVGGCHFAEVQVREKATG 124  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPHPIQLOAFQDKNHLXLYLWMEYQPGG 180  
DB 125 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPHPIQLOAFQDKNHLXLYLWMEYQPGG 184  
QY 181 DLLSLNRYEDQDENLQIYLAELILAVHSVHLMGVHRDIKFNILVDRTGHIKLVDF 240  
DB 185 DLLSLNRYEDQDENLQIYLAELILAVHSVHLMGVHRDIKFNILVDRTGHIKLVDF 244  
QY 241 GSAAKMNSNPOVNAKPIGTPDYMPEVLTVMGDGKGYGLDCDWSVGVIAYENIYGR 300  
DB 245 GSAAKMNSNPOVNAKPIGTPDYMPEVLTVMGDGKGYGLDCDWSVGVIAYENIYGR 304  
QY 301 SPFAEGTSATFNINMNFQRLKFPDDPKVSSDFDLIQLSLGCGKRLKFEGLCCHPFF 360  
DB 305 SPFAEGTSATFNINMNFQRLKFPDDPKVSSDFDLIQLSLGCGKRLKFEGLCCHPFF 364  
QY 361 SKIDWNINRSPFPFVPTLKSDDDTNSNFDPEKNVSWSSPCQLSPSGSGSGBELPVGFS 420  
DB 365 SKIDWNINRSPFPFVPTLKSDDDTNSNFDPEKNVSWSSPCQLSPSGSGSGBELPVGFS 424

QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 472

RESULT 9

ADAO5644 standard; protein; 623 AA.

AC ADA05644;

DT 06-NOV-2003 (first entry)

DE Human NOV1b protein SEQ ID NO:4.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
XX immunomodulator; cytostatic; nootropic; neuroprotective;  
XX antiparkinsonian; antilipaeamic; gene therapy; human disease;  
XX metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
XX immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

PN WO2003029424-A2.

XX 10-APR-2003.

PD 02-OCT-2002; 2002WO-US031373.

PF 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 17-APR-2002; 2002US-0373260P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.

PR 19-APR-2002; 2002US-0373826P.

PR 19-APR-2002; 2002US-0373884P.

PR 22-APR-2002; 2002US-0374977P.

PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.

PR 17-MAY-2002; 2002US-0381042P.

PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;  
PI Ort T, Gorman L, Zerhusen SD, Anderson DW, Zhong M, Catterton E;  
PI Ji W, Miller CE, Rastelli L, Stone DU, Pena CE, Shenoy SG;  
PI Shimkets RA, Rotherberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI: 2003-381626/36.

DR N-PSDB; ADA05644.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,  
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,  
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Claim 1; Page 100-101; 586pp; English.  
XX  
CC The present invention describes NOVX proteins, where X can be 1 to 55  
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide  
CC described above and a carrier; (2) a kit comprising, in one or more  
CC containers, the composition described above; (3) an isolated nucleic acid  
CC molecule which encodes a NOVX protein of the invention; (4) a vector  
CC comprising the nucleic acid molecule described above; (5) a cell  
CC comprising the above vector; (6) an antibody that immunospecifically  
CC binds to the polypeptide described above; (7) methods for determining the  
CC presence or amount of the above polypeptide or nucleic acid molecule in a  
CC sample; (8) methods for determining the presence of or predisposition to  
CC a disease associated with altered levels of expression of the above  
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a  
CC method of identifying an agent that binds to the polypeptide described  
CC above; (10) a method for identifying a potential therapeutic agent for  
CC use in treating a pathology that is related to an aberrant expression or  
CC aberrant physiological interactions of the polypeptide; (11) a method of  
CC screening for a modulator of activity of or of latency or predisposition to  
CC a pathology associated with the polypeptide; (12) a method for modulating  
CC the activity of the polypeptide described above; (13) methods of treating  
CC or preventing a pathology associated with the above polypeptide in a  
CC mammal; and (14) a method for producing the above polypeptide. NOVX  
CC sequences have antidiabetic, anorectic, antibacterial, virucide,  
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian  
CC and antilipidemic activities, and can be used in gene therapy. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease. The polypeptide or the nucleic  
CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, haematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a human NOVX from the  
CC present invention.  
XX

SQ Sequence 623 AA;

Query Match 93.8%; Score 2440; DB 6; Length 623;  
Best Local Similarity 99.6%; Pred. No. 8.2e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60  
Db 5 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 64  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVREKATG 120  
Db 65 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVREKATG 124  
QY 121 DIYAMKVMKKKALLAQOVSFFEEERNILSRSPWIPOLQYAFQDKXHLVLMVEYOPGG 180  
Db 125 DIYAMKVMKKKALLAQOVSFFEEERNILSRSPWIPOLQYAFQDKXHLVLMVEYOPGG 184  
QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVLMGYVHRDIKPENILVDRTHGKLVDF 240  
Db 185 DLLSLNRYEDQDLENLIQFYLAELILAVHSVLMGYVHRDIKPENILVDRTHGKLVDF 244  
QY 241 GSAKXNSKNWNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDWWSGVYAYEMIVGR 300  
Db 245 GSAKXNSKNWNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDWWSGVYAYEMIVGR 304  
QY 301 SPFAEGTSARTNNIMNFQRLKFPDDPKVSSDFDLIQSLCCGQKRLKFGGLCCHPFF 360  
Db 305 SPFAEGTSARTNNIMNFQRLKFPDDPKVSSDFDLIQSLCCGQKRLKFGGLCCHPFF 364

QY 361 SKIDWNINRNSPPFPVFTLKSDDDTSNDEPEKNSWSSSPCOLSPSGSGELPVGFS 420  
Db 365 SKIDWNINRNSPPFPVFTLKSDDDTSNDEPEKNSWSSSPCOLSPSGSGELPVGFS 424  
QY 421 YSKALGILGRSBSVSGLDSPAKTSMEKLLIKSKELQDSQDKCHKV 468  
Db 425 YSKALGILGRSBSVSGLDSPAKTSMEKLLIKSKELQDSQDKCHKV 472

RESULT 10

ABB81928

ID ABB81928 standard; protein; 1958 AA.

XX ABB81928;

DT 10-OCT-2002 (first entry)

DE Human kinase #2.

XX Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.

OS Homo sapiens.

XX WO200259325-A2.

PD 01-AUG-2002.

XX 20-DEC-2001; 2001WO-US050497.

XX 27-DEC-2000; 2000US-0258335P.

PA (LEXI-) LEXICON GENETICS INC.

PI Yu X, Miranda M, Friddle CJ;

DR WPI: 2002-599796/54.

XX N-PSDB; ABQ78871.

Novel polynucleotide encoding human proteins that are structurally  
PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
PT applications.  
XX  
PS Claim 4; Page 46-50; 50pp; English.  
XX  
CC The invention relates to a novel human protein that shares structural  
CC similarity with animal kinases, including serine-threonine kinases,  
CC particularly Citron rho-interacting kinases. The proteins of the  
CC invention have nootropic and cytostatic activity. The polynucleotides may  
CC have a use in gene therapy. The encoded novel polypeptides are useful for  
CC generating antibodies, as reagents in diagnostic assays, for identifying  
CC other cellular gene products related to NHP and as reagents in assays for  
CC screening for compounds that are useful in the treatment of mental,  
CC biological or medical disorders and diseases including cancer. The  
CC sequence represents a novel human kinase of the invention

SQ Sequence 1958 AA;

Query Match 93.8%; Score 2440; DB 5; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5.4e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVREKATG 120  
Db 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVREKATG 120  
QY 121 DIYAMKVMKKKALLAQOVSFFEEERNILSRSPWIPOLQYAFQDKXHLVLMVEYOPGG 180



Db 121 DIYAMKVMKKALLAQEQVFFEEERNILSRSTSPWIPQLOAFQDKNHLVLMVEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNKNVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMVYGR 300  
 Db 241 GSAAKNSNKNVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMVYGR 300  
 QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLCGKRLKEGCLCHPFF 360  
 Db 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLCGKRLKEGCLCHPFF 360  
 QY 361 SKIDWNINRNSPPFPVPTLKSDDTSNFEPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
 Db 361 SKIDWNINRNSPPFPVPTLKSDDTSNFEPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 11  
 ABB81927  
 ID ABB81927 standard; protein; 2054 AA.  
 XX AC ABB81927;  
 DT 10-OCT-2002 (first entry)  
 XX DE Human kinase #1.  
 XX KW Human; kinase; enzyme; serine-threonine kinase; neutrotropic; cytosolic;  
 KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.  
 XX OS Homo sapiens.  
 XX PN WO200259325-A2.  
 XX PD 01-AUG-2002.  
 XX PF 20-DEC-2001; 2001WO-US050497.  
 XX PR 27-DEC-2000; 2000US-0258335P.  
 XX PA (LEXI-) LEXICON GENETICS INC.  
 XX PI Yu X, Miranda M, Friddle CJ;  
 XX WPI; 2002-599796/64.  
 XX DR N-PSDB; ABQ78870.  
 XX Novel polynucleotide encoding human proteins that are structurally  
 PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
 PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
 PT applications.  
 XX Claim 2; Page 39-43; 50pp; English.  
 XX The invention relates to a novel human protein that shares structural  
 CC similarity with animal kinases, including serine-threonine kinases,  
 CC particularly Citron rho-interacting kinases. The proteins of the  
 CC invention have neutrotropic and cytosolic activity. The polynucleotides may  
 CC have a use in gene therapy. The encoded novel polypeptides are useful for  
 CC generating antibodies, as reagents in diagnostic assays, for identifying  
 CC other cellular gene products related to NHP and as reagents in assays for  
 CC screening for compounds that are useful in the treatment of mental,  
 CC biological or medical disorders and diseases including cancer. The  
 CC sequence represents a novel human kinase of the invention  
 XX Sequence 2054 AA;  
 SQ

Query Match 93.8%; Score 2440; DB 5; Length 2054;  
 Best Local Similarity 99.6%; Pred. No. 5.8e-237;  
 Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRSLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIASRSLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDTIABLOLQPSAKDFEVRSLVGGCHFAEQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIABLOLQPSAKDFEVRSLVGGCHFAEQVREKATG 120  
 QY 121 DIYAMKVMKKALLAQEQVFFEEERNILSRSTSPWIPQLOAFQDKNHLVLMVEYQPGG 180  
 Db 121 DIYAMKVMKKALLAQEQVFFEEERNILSRSTSPWIPQLOAFQDKNHLVLMVEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNKNVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMVYGR 300  
 Db 241 GSAAKNSNKNVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMVYGR 300  
 QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLCGKRLKEGCLCHPFF 360  
 Db 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLCGKRLKEGCLCHPFF 360  
 QY 361 SKIDWNINRNSPPFPVPTLKSDDTSNFEPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
 Db 361 SKIDWNINRNSPPFPVPTLKSDDTSNFEPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 12  
 AAE24150  
 ID AAE24150 standard; protein; 2054 AA.  
 XX AC AAE24150;  
 DT 23-SEP-2002 (first entry)  
 XX DE Human kinase (PKIN)-21 protein.  
 XX KW Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;  
 KW acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;  
 KW asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;  
 KW development; hepatitis; cardiovascular; hypertension; drug screening;  
 KW myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;  
 KW fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;  
 KW hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hiv;  
 KW neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;  
 KW hyperlipidaemia; enzyme.  
 XX OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Domain 97..360  
 FT Domain /note= "Eukaryotic protein kinase domain"  
 FT Domain 98..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 99..349  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 101..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 102..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 249..349  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 258..445

FT Domain /note= "Protein kinase domain"  
 FT 258..349  
 FT /note= "Protein kinase domain"  
 FT 534..542  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 854..875  
 FT /note= "Leucine zipper pattern"  
 FT 891..933  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 964..975  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 991..1012  
 FT /note= "Leucine zipper pattern"  
 FT 1015..1067  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1057..1078  
 FT /note= "Leucine zipper pattern"  
 FT 1159..1180  
 FT /note= "Leucine zipper pattern"  
 FT 1217..1255  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1388..1434  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1330..1438  
 FT /note= "Phorbol esters/diacylglycerol binding site"  
 FT 1403..1466  
 FT /note= "Phorbol esters/diacylglycerol binding site"  
 FT 1471..1590  
 FT /note= "PH domain"  
 FT 1619..1916  
 FT /note= "CNH domain"  
 FT 1759..1802  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1819..1831  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1851..1880  
 FT /note= "Domain found in NIK1-like kinase"  
 XX  
 PN WO200233099-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 20-OCT-2001; 2001WO-US047728.  
 XX  
 PR 20-OCT-2000; 2000US-0242410P.  
 PR 27-OCT-2000; 2000US-0240568P.  
 PR 03-NOV-2000; 2000US-0245708P.  
 PR 09-NOV-2000; 2000US-0247672P.  
 PR 16-NOV-2000; 2000US-0249565P.  
 PR 22-NOV-2000; 2000US-0252730P.  
 PR 01-DEC-2000; 2000US-0250807P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;  
 PI Gao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;  
 PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;  
 PI Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;  
 PI Thangavelu K, Khan PA, Ison CH;  
 XX  
 DR WPI: 2002-454603/48.  
 DR N-PSDB: AAD38864.  
 XX  
 XX New human kinase polypeptide, for diagnosing, preventing and treating  
 FT cancer, immune system disorders, growth and development disorders,  
 FT cardiovascular disorders and lipid disorders.  
 PT  
 XX  
 PS Claim 1; Page 177-182; 210pp; English.  
 XX  
 CC The invention relates human kinases (PKIN) and their corresponding  
 CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing  
 CC treating and preventing cancer, an immune system disorder (e.g., acquired  
 CC immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting  
 CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),  
 CC cardiovascular disorder (e.g., hypertension, myocardial infarction,  
 CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,  
 CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,  
 CC hyperlipidaemia, obesity), and for assessing the effects of exogenous  
 CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a  
 CC condition or a disease associated with the expression of PKIN in a  
 CC biological sample. A composition comprising PKIN or an agonist or  
 CC antagonist of PKIN is useful for treating a disease or condition  
 CC associated with decreased or increased expression of functional PKIN.  
 CC PKIN is useful in a number of drug screening techniques and to analyse  
 CC the proteome of a tissue or cell type. PKIN DNA is useful for creating  
 CC knockin humanised animals or transgenic animals to model human diseases,  
 CC and in somatic or germline gene therapy. The present sequence is human  
 CC PKIN protein  
 XX  
 SQ Sequence 2054 AA;  
 Query Match 93.8%; Score 2440; DB 5; Length 2054;  
 Best Local Similarity 99.6%; Pred. No. 5.8e-237;  
 Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLPFGQPPFPMTQOQMSPLSREGILDALFVLFE 60  
 DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLPFGQPPFPMTQOQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSNFVRKYSDDTTAELOELQPSAKDFEVRSLVCGGHAQVQVREKATG 120  
 DB 61 ECSQPALMKIKHVSNFVRKYSDDTTAELOELQPSAKDFEVRSLVCGGHAQVQVREKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSEFEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
 DB 121 DIYAMKVMKKKALLAQEQVSEFEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHKLVDFF 240  
 DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHKLVDFF 240  
 QY 241 GSAAKMSNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 DB 241 GSAAKMSNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMVYGR 300  
 QY 301 SPFAEGTSARTFNINMFQRLKFPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMFQRLKFPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPQSPGSGEELPFVGFPS 420  
 DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPQSPGSGEELPFVGFPS 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 RESULT 13  
 AAO26959  
 ID AAO26959 standard; protein; 2054 AA.  
 XX  
 AC AAO26959;  
 XX  
 XX  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE Human CRK protein sequence, SEQ ID No 2.  
 XX  
 KW Anorectic; hypotensive; cardiant; antilipaeamic; cerebroprotective;  
 KW antitumor; osteopathic; antiarthritic; cytostatic; antidepressant;  
 KW immunomodulator; antitumor; tranquiliser; antiparkinsonian; nootropic;  
 KW neuroprotective; antiinflammatory; antidiabetic; analgesic;  
 KW human cirron rho/rac-interacting kinase; enzyme; CRK; ameliorating;  
 KW obesity; comorbidity; cancer; anorexia; cachexia; bulimia;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;

diabetes; pain.  
Homo sapiens.  
WO2003004523-A1.  
16-JAN-2003.  
28-JUN-2002; 2002WO-EP007156.  
02-JUL-2001; 2001US-0301841P.  
11-DEC-2001; 2001US-0338651P.  
25-APR-2002; 2002US-0375014P.  
(FARB ) BAYER AG.  
Zhu Z;  
WPI; 2003-221576/21.  
N-PSDB; AAL55214.  
New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or Alzheimer's disease.  
Claim 1; Fig 2; 237pp; English.  
The invention relates to an isolated polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer), anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This sequence represents the human CRIK protein of the invention

Query Match 93.8%; Score 2440; DB 6; Length 2054;  
Best Local Similarity 99.6%; Pred. No. 5.8e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRFKYGARNPLDAGAAEPIANRSLNLFQCKPPFTQQQMSPLSRGILDALFVLFE 60  
Db 1 MLRFKYGARNPLDAGAAEPIANRSLNLFQCKPPFTQQQMSPLSRGILDALFVLFE 60  
QY 61 ECSPALMKIKHVSFNVRKYSIDTIAELOQLPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
Db 61 ECSPALMKIKHVSFNVRKYSIDTIAELOQLPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
QY 121 DIYAMVKMKKALLAQEQVSEFFERNILSRSTSPWIPOLQAFQDNHLYLVMEYQPG 180  
Db 121 DIYAMVKMKKALLAQEQVSEFFERNILSRSTSPWIPOLQAFQDNHLYLVMEYQPG 180  
QY 181 DILSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDKPENILVDRTHGKLVDF 240  
Db 181 DILSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDKPENILVDRTHGKLVDF 240

QY 241 GSAAKNSNKNVNAKLPICTPDYMAPEVLTVANGDGKGTGYGLDCDWSVGVYAYEMIYGR 300  
Db 241 GSAAKNSNKNVNAKLPICTPDYMAPEVLTVANGDGKGTGYGLDCDWSVGVYAYEMIYGR 300  
QY 301 SPFAEGTSARTNNINNFORFLKFPDDPKVSSDFLDLIQSLLCGOKERLKPEGLCCHPFF 360  
Db 301 SPFAEGTSARTNNINNFORFLKFPDDPKVSSDFLDLIQSLLCGOKERLKPEGLCCHPFF 360  
QY 361 SKIDMNNIRNSPPFPVFTLKSDDDTSNFDPEPKNSWVSSPCQLSPSGFSGBELFVGFS 420  
Db 361 SKIDMNNIRNSPPFPVFTLKSDDDTSNFDPEPKNSWVSSPCQLSPSGFSGBELFVGFS 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSODKCHKV 468  
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSODKCHKV 468

RESULT 14  
AAE24079  
ID AAE24079 standard; protein; 2053 AA.  
XX  
AC AAE24079;  
XX  
DT 04-OCT-2002 (first entry)  
XX  
DE Human MDPK protein.  
XX  
KW Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein; tumourigenesis; tumour growth; tumour metastasis; viral infection; skeletal muscle disorder; muscular dystrophy; myotonic dystrophy; immune disorder; neoplastic disorder; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 53..303 /note= "pkinase domain"  
FT Domain 97..360 /note= "pkinase domain"  
FT Region 195..210 /note= "Antigenic epitope"  
FT Region 217..229 /note= "Serine/Threonine protein kinase active site signature"  
FT Region 455..475 /note= "Antigenic epitope"  
FT Domain 1588..1865 /note= "CNH domain"  
XX  
PN WO200234896-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 23-OCT-2001; 2001WO-US0505636.  
XX  
PR 23-OCT-2000; 2000US-0242429P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Kapeller-Libermann R;  
XX  
DR WPI; 2002-479720/51.  
XX  
DR N-PSDB; AAD39191.  
XX  
PT Human myotonic dystrophy type protein kinase polypeptide and polynucleotide useful for prognosticating, diagnosing, preventing or inhibiting tumorigenesis, tumor growth, tumor metastasis and viral infection.  
XX  
PS Claim 8; Fig 3; 148pp; English.  
XX  
CC The invention relates to human myotonic dystrophy type protein kinase

CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules  
 CC encoding such polypeptides. 13245 molecules are used to develop  
 CC diagnostic and therapeutic agents for prognosticating, diagnosing,  
 CC preventing, inhibiting, alleviating or curing MDPK-related disorders.  
 CC Polypeptides of the invention are used to develop diagnostic and  
 CC therapeutic agents for 13245-mediated or related disorders such as  
 CC tumorigenesis, tumour growth, tumour metastasis, viral infection of a  
 CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),  
 CC immune disorders and neoplastic disorders. The invention is also used in  
 CC gene therapy. The present sequence is human MDPK protein  
 XX  
 XX Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 5; Length 2053;  
 Best Local Similarity 99.1%; Pred. No. 6e-236;  
 Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 Db 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKMNSKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDMSVGVIAVEMIGR 300  
 Db 241 GSAAKMNSKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDMSVGVIAVEMIGR 300  
 QY 301 SPFAEGTSARTFNINMNFQRLKFPDDPKYSSDFLDLIQSLGQKERLKFGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNINMNFQRLKFPDDPKYSSDFLDLIQSLGQKERLKFGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGBELPVGFS 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGBELPVGFS 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

RESULT 15  
 ADF60994  
 ID ADF60994 standard; protein; 2053 AA.  
 XX  
 AC ADF60994;  
 XX

DT 12-FEB-2004 (first entry)  
 DE Pain associated human 2207 polypeptide.  
 XX

KW Pain modulation; pain disorder; painful disorder; potassium channel;  
 KW kinase expression; inflammatory pain; chronic pain; neuropathic pain;  
 KW causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;  
 KW analgesic; antiinflammatory.

OS Homo sapiens.  
 XX  
 XX US2003153525-A1.  
 XX  
 XX 14-AUG-2003.  
 XX  
 XX 19-DEC-2002; 2002US-00325430.  
 XX

PR 19-DEC-2001; 2001US-0341953P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Silos-Santiago I, Rosenfeld JB,  
 PI  
 XX WPI; 2003-897732/82.  
 DR N-PSDB; ADF60992, ADF60993.  
 XX  
 PT Identifying a compound capable of treating a pain disorder comprises  
 PT assaying the ability of the compound to modulate specific, e.g., kinases  
 PT or potassium channel, nucleic acid expression or polypeptide activities.  
 XX  
 XX Disclosure; SEQ ID NO 12; 80pp; English.  
 PS  
 XX The present invention relates to a method for identifying a compound  
 CC capable of modulating pain or painful disorders. The method comprises  
 CC assaying the ability of the compound to modulate specific nucleic acid  
 CC expression or polypeptide activity e.g. potassium channel, or kinase  
 CC expression/activity. The method and compounds are useful for treating  
 CC pain or painful disorders e.g. inflammatory pain, chronic pain,  
 CC neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache  
 CC pain and tissue pain. The present sequence represents a human protein  
 CC associated with pain.  
 XX  
 SQ Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 7; Length 2053;  
 Best Local Similarity 99.1%; Pred. No. 6e-236;  
 Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 Db 61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKMNSKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDMSVGVIAVEMIGR 300  
 Db 241 GSAAKMNSKNVNAKLPIGTDPYMAPEVLTVMNGDGKGTGLDCDMSVGVIAVEMIGR 300  
 QY 301 SPFAEGTSARTFNINMNFQRLKFPDDPKYSSDFLDLIQSLGQKERLKFGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNINMNFQRLKFPDDPKYSSDFLDLIQSLGQKERLKFGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGBELPVGFS 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGBELPVGFS 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

Search completed: November 8, 2004, 12:28:13  
 Job time : 160 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 04:16:56 ; Search time 4438 seconds  
(without alignments)  
12439.431 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 9999gagatgtgaagttcaa.....tctgagcgcctgacgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_est4:  
5: gb\_est5:  
6: gb\_est6:  
7: gb\_est7:  
8: gb\_est8:  
9: gb\_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.6	39.8	698	5	BP146990
2	521.2	34.4	1085	4	BM904785
3	452.8	29.9	600	4	EG808136
4	423.8	28.0	427	4	EG944539
5	413.2	27.3	617	5	BQ417810
6	380	25.1	481	7	CN682405
7	378	25.0	479	7	CN678533
8	351.4	23.2	490	4	BF562826
9	344.2	22.7	821	4	BF562822
10	329.2	21.7	450	9	CG501400
11	328.8	21.7	423	3	BF344814
12	327	21.6	449	9	CG501399
13	318.2	21.0	512	9	CG52891
14	314.2	20.7	340	2	BF380737
15	312.6	20.6	582	5	BX516231
16	281.6	18.6	521	1	AI882189
17	281.4	18.6	355	8	CG325092
18	278.8	18.4	539	3	AW525215
19	276.4	18.2	325	3	BC008127
20	272.6	18.0	336	9	CG869028
21	270.8	17.9	321	2	BF932611
22	262.4	17.3	335	2	BF763211
23	262.4	17.3	524	7	CK841805
24	251.8	16.6	423	2	BB827314

25	251.4	16.6	398	5	BY018641
26	246.2	16.3	385	9	CG555761
27	246.2	16.3	289	9	BF944809
28	246	16.2	508	6	CB783081
29	245.8	16.2	547	7	CF744826
30	245.8	16.2	647	7	CF744826
31	244.8	16.2	801	5	BU475240
32	244.8	16.2	847	5	BU475240
33	243.4	16.1	907	7	CK147448
34	240.8	15.9	401	5	BY602044
35	238.8	15.8	2688	3	BC024150
36	237.2	15.7	2862	3	BC056615
37	236	15.6	1478	9	AY408842
38	233.6	15.4	605	5	BP168081
39	233.4	15.4	563	6	CD310316
40	231.6	15.3	370	5	BY021399
41	231.4	15.3	423	2	BB823725
42	225.2	14.9	1600	3	BC038993
43	222	14.7	400	1	AL360718
44	219.4	14.5	525	2	BF558465
45	218.4	14.4	1472	9	AY408840

ALIGNMENTS

RESULT 1  
LOCUS BP146990 698 bp mRNA linear EST 30-DEC-2003  
DEFINITION BP146990 full-length enriched swine cDNA library, adult ovary Sus  
ACCESSION BP146990  
VERSION BP146990.1 GI:40396461  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
REFERENCE 1 (bases 1 to 698)  
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Okumura, N., Hamasima, N. and Awata, T.,  
Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,  
PEDE (Pig EST Data Explorer): construction of a database for ESTs  
derived from porcine full-length cDNA libraries  
Nucleic Acids Res. 32 (1), D484-D488 (2004)  
JOURNAL Contact: Hirohide Unishi  
COMMENT Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAPF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

FEATURES  
source 1..698  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="OVRM10025B09"  
/tissue\_type="ovary"  
/dev\_stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult ovary"  
ORIGIN  
Query Match 39.8%; Score 602.6; DB 5; Length 698;  
Best Local Similarity 91.4%; Pred. No. 2.8e-172;





REFERENCE 1 (bases 1 to 600)  
 AUTHORS Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.  
 TITLE Gene expression in the developing mouse retina by EST sequencing and microarray analysis  
 JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
 MEDLINE 21671825  
 PUBMED 11812828  
 COMMENT Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329

FEATURES  
 Location/Qualifiers  
 1..600  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /tissue\_type="neural retina"  
 /dev\_stage="embryonic day 14.5 post-fertilization"  
 /clone\_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN  
 Query Match 29.9%; Score 452.8; DB 4; Length 600;  
 Best Local Similarity 86.6%; Pred. No. 1.8e-126;  
 Matches 499; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 GGGAGATGTTGAAGTTCAAATATGGAGCGCGAATCTTTGGATCTGTGCTGCGAA 60  
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 Db 25 GGAGAGATGTTGAAGTTCAGATGTTGTCGGAAACCGCGGAGCGAGTCTCCGAG 84  
 |||||  
 QY 61 CCCATTGCCAACCGGCTCCAGCTGAATCTCTTCTCCAGGGGAACACCCCTTATG 120  
 |||||  
 Db 85 CCCATTGCCAGTCGGGCTCCAGCTAAATCTCTTCTCCAGGGGAACCGCCCTCATG 144  
 |||||  
 QY 121 ACTCAACAGCAGATGTCCTCTTTCGCCGAGAGGATATTAGATGCCCTCTTTGTCTC 180  
 |||||  
 Db 145 ACTCAACAGCAGATGTCCTCTTTCGCCGAGAGGATGTCAGACGCCCTCTTCGCTCTC 204  
 |||||  
 QY 181 TTTGAAGATGTCAGTCAGCTCTGTATGAAGATTAAGCAGTGAACACTTTGTCGG 240  
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 Db 205 TTTGAAGATGTCAGTCAGCTCTGTATGAAGATTAAGCAGTGAACACTTTGTCGG 264  
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 QY 241 AAGTATTCCACACCATAGCTGATGAGTACAGGACTCCAGCTTCGCAAGAGACTTCGAA 300  
 |||||  
 Db 265 AAGTATTCCACACCATAGCTGAGTTCGCGAGCTCGAGCGCTCGCGGAGACTTCGAA 324  
 |||||  
 QY 301 GTCAGAGCTTTGTAGTTGTGTCTCTTTGCTGAAGTGCAGTGTGAAGAGAAAGCA 360  
 |||||  
 Db 325 GTTCGAGGCTTTGTGGCTGTGCTCACTTCGCTGAAGTGCAGTGTGTGAAGAGAGGG 384  
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 QY 361 ACCGGGACATCTATGCTATGAAGTGCATGAAGAGAGAGGCTTATTCGCCAGGAGCG 420  
 |||||  
 Db 385 ACCGGGACATCTATGCTATGAAGTGCATGAAGAGAGAGGCTTATTCGCCAGGAGCG 444  
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 QY 421 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 480  
 |||||  
 Db 445 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGGAGCAGAGTCTTGGATCCCC 504  
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 QY 481 CAATTACAGTATGCTTTTCAGGCAAAATATCCTTTATCTGTGTATGGAATATACGCT 540  
 |||||  
 Db 505 CAGTTACAGTATGCTTTTCAGGCAAAATATCCTTTTACCTGTGTATGGAATATACGCT 564  
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 QY 541 GGAGGGGACTTGTGTCTACCTTTTGAATAGATATGAG 576  
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 Db 565 GGAGGGGACTTGTGTCTTCTTGAACAGATACGAG 600  
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RESULT 4  
 BG944539  
 LOCUS  
 DEFINITION ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library) EST 15-JAN-2003

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

FEATURES  
 source

Homo sapiens cDNA clone ax51f11 random, mRNA sequence.  
 BG944539  
 BG944539.1 GI:14343911  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.  
 Gene expression in proliferating human erythroid cells  
 Genomics 59 (2), 168-177 (1999)  
 99339981  
 10409428  
 Contact: Jeffery L. Miller  
 Laboratory of Chemical Biology  
 National Institute of Diabetes and Digestive and Kidney Diseases  
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD  
 20892, USA  
 Tel: 301 402 2373  
 Fax: 301 435 5148  
 Email: jml@nih.gov  
 DNA Sequencing and analyses by National Institutes of Health  
 Intramural Sequencing Center (NISC).  
 Plate: 51 row: f column: 11  
 Seq primer: -21M13 forward primer (ABI).  
 Location/Qualifiers  
 1..427  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ax51f11"  
 /sex="unknown"  
 /tissue\_type="blood"  
 /cell\_type="Erythroid Cells"  
 /cell\_line="Primary Culture of Peripheral Blood Mononuclear Cells"  
 /dev\_stage="Progenitor; EPO responsive CD71+""  
 /lab\_host="SOLR"  
 /clone\_lib="Hembase; Erythroid Progenitor Cells (LCB:ax library)"  
 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: EcoRI; 65,000 proliferating erythroid cells from the Buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."

ORIGIN

Query Match 28.0%; Score 423.8; DB 4; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-117;  
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 148 CGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATCGAGTCAGCTGCTCTG 207  
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 Db 1 CGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATCGAGTCAGCTGCTCTG 60  
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 QY 208 ATGAAGATTAAGCAGGTGAGCACTTTGTCGGAGTATTCGACACCATAGCTGAGTTA 267  
 |||||  
 Db 61 ATGAAGATTAAGCAGGTGAGCACTTTGTCGGAGTATTCGACACCATAGCTGAGTTA 120  
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 QY 268 CAGGAGCTCCAGCTTCGGCAAGAGACTTCGAAGTCAGAAGTCTTTGTTAGTTGGTTCAC 327  
 |||||  
 Db 121 CAGGAGCTCCAGCTTCGGCAAGAGACTTCGAAGTCAGAAGTCTTTGTTAGTTGGTTCAC 180  
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328 TTGCTGAAGTCAAGTGTGTAAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTG 387  
 181 TTGCTGAAGTCAAGTGTGTAAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTG 240  
 388 ATGAAGAAGAGGCTTTATTGGCCCGAGGAGGAGTTTCAATTTTGGAGAGAGCGGAAC 447  
 241 ATGAAGAAGAGGCTTTATTGGCCCGAGGAGGAGTTTCAATTTTGGAGAGAGCGGAAC 300  
 448 ATATTATCTCGAGACACAGCCGGTGGATCCCGCAATACAGTATGCTTTCAGACAAA 507  
 301 ATATTATCTCGAGTACAGCCCGGATCCCGCAATACAGTATGCTTTCAGACAAA 360  
 508 AATCACTTTATCTGCTGATGAATATACAGCTCGAGGGGACTTCTGCTCACTTTTGAAT 567  
 361 AATCACTTTATCTGCTGATGAATATACAGCTCGAGGGGACTTCTGCTCACTTTTGAAT 420  
 568 AGATATG 574  
 421 AGATATG 427

RESULT 5  
 BQ417810  
 LOCUS  
 DEFINITION  
 BQ417810.1 GI:21123011  
 Mus musculus (house mouse)  
 EST.  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 617)  
 Lemshka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisclair, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,  
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,  
 Williams, T., Jackson, Y. and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biochem.harvard.edu  
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,  
 2000) Library was constructed by Catherine Lee DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Marie Searce  
 (mscarce@mail.med.upenn.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 367.  
 Location/Qualifiers  
 1. .617

FEATURES  
 source  
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 /clone\_lib="Kaestner ngn3 wt"  
 /notes="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site\_1:  
 Not 1; Site 2: Sal I; The library was prepared by  
 Catherine S. Lee and has not been published. The pancreas  
 was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,  
 2000). The cdna's were prepared with an oligo containing a

ORIGIN  
 Query Match 27.3%; Score 413.2; DB 5; Length 617;  
 Best Local Similarity 86.1%; Pred. No. 2.3e-114;  
 Matches 457; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
 QY 1 GGGAGATGTTGAAGTTCATATATGAGCGCGGAATCCCTTGGATGCTGCTGCTGAA 60  
 DB 87 GGAAGATGTTGAAGTTCATATATGAGCGCGGAATCCCTTGGATGCTGCTGCTGAA 146  
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 DB 147 CCCATTGCCAGTCCGGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTATG 206  
 QY 121 ACTCAACAGCAGATGCTCTCTTCCCGAAGAGGATATAGATGCTCTTCTTCTC 180  
 DB 207 ACTCAACAGCAGATGCTCTCTTCCCGAAGAGGATATAGATGCTCTTCTTCTC 266  
 QY 181 TTTGGAAGATGAGTCAAGTCTGCTGATGAAGATTAAAGCACTGAGCAACTTTGTCGG 240  
 DB 267 TTTGGAAGTGAAGCAACCCCGCTGATGAAGATGAAGCACTGAGCAAGTTTGTCCAG 326  
 QY 241 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAA 300  
 DB 327 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAA 386  
 QY 301 GTCAGAAGTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 DB 387 GTTCAGAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446  
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 DB 447 ACCGGGACATCTATGCTGATGAAGTGAAGCAAGAGGCTTTATTTGGCCCGAGGACAG 506  
 QY 421 GTTTCATTTTTCAGAGAGCGGACATATATTCGAGCAAGACCGGTTGATTCCTCC 480  
 DB 507 GTTTCATTTTTCAGAGAGCGGACATATATTCGAGCAAGACCGGTTGATTCCTCC 566  
 QY 481 CAATTACAGTATGCTTTCAGGACAAATATCACTTTATCTGCTGCTGCTGCTGCTGCTG 531  
 DB 567 CAGTTACAGTATGCTTTCAGGACAAATATCACTTTATCTGCTGCTGCTGCTGCTGCTG 617

RESULT 6  
 CN682405  
 LOCUS  
 DEFINITION  
 E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low  
 density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04  
 IMAGE:30782511 5', mRNA sequence.  
 CN682405  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 481)  
 Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,  
 Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,  
 Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,  
 Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,  
 Schllessinger, D., Keller, J., Klotz, E., Kelsey, G., Umezawa, A.,  
 Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,  
 D'Urso, M., Kelsey, J., Hide, W. and Ko, M.S.  
 Transcription analysis of mouse stem cells and early embryos  
 PLOS Biol. 1 (3), 410-419 (2003)  
 Contact: Dawood B. Dudekula

NotI site, and SalI linkers were added to the ends. The  
 inserts were cut with NotI before being cloned into the  
 NotI-SalI sites in the vectors. This is one of two  
 libraries, ngn3 wt and ngn3 -/- . The wt library is in  
 pSPORT1, 17 promoter is 5'."

Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: E0164 row: B column: 04  
Seq primer: M13 Reverse  
High quality sequence stop: 481  
POLYA=No.

FEATURES  
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1. .481  
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/clone="NIA:E0164B04 IMAGE:30782511"  
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/tissue\_type="Embryonic Stem Cell"  
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/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long)"  
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x103/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen]: 5'-pGACTAGTTCGATCGGAGCGCGCCCTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

ORIGIN  
Query Match 25.1%; Score 380; DB 7; Length 481;  
Best Local Similarity 88.0%; Pred. No. 3.1e-104;  
Matches 426; Conservative 0; Mismatches 55; Indels 3; Gaps 1;  
QY 297 CGAAGTCAGAAGTCTTGTAGGTTGGTCTACTTTGTGTAAGTCAGCGGTGTAGAGAGAA 356  
DB 1 CGAAGTTCGAAGCCTTGTGGGCTGTGCTCACTTCGCTGAAGTCAGGTGTAGAGAGAA 60  
QY 357 AGCAACCGGGACATCTATCTATGAAGTGATGAAGAGAGAGCGTTTATTTGGCCCGAGGA 416  
DB 61 GGGACCGGGAGCGCTATGCCATGAATAATCATGAAGAGAGAGCGTTTGTGGCCCGAGGA 120  
QY 417 GCAGGTTTCATTTTTTGGAGGAGCGGAGACATATTATCTCGAGCAGCAGCGCGGTGGAT 476  
DB 121 ACAGGTTTCATTTTTTGGAGGAGAGAGAGACATATTATCTCGAGCAGCAGCGGTGGAT 180  
QY 477 CCCCCAATTACAGTATCCCTTCAGGACAAATACCTTTATCTGGTCAATGAATATCA 536  
DB 181 CCCCCAGTTACAGTACCGCTTCAGGACAAATATACCTTTTACCTGGTCAATGAATATCA 240  
QY 537 GCCTGGAGGGGACCTTGTGTCACCTTTTGAATAGATATGAGGACAGTTCAGTAAACCT 596

Db 241 CCCTGGAGGGGATTGCTGTGCTTCTGAACAGATACGAGGACCAATTAGATGAGACAT 300  
QY 597 GATACAGTTTTTACCTAGCTAGCTGATTTGGTGTGTTTCACAGCGTTTCATCTGATGGGATA 656  
Db 301 GATCAGTTTTTACCTTGTGCTGATGATTTGGTGTGTTTCACAGCGTGCACCATGATGGGATA 360  
QY 657 CGTCATCGAGACATCAAGCCTGAGAACATCTCTGTTGACCGCACAGACACATCAAGCT 716  
Db 361 TGTGATCGAGACATCAAGCCCGAGAACATCTCTATCGCCGACGGGACACATCAAGCT 420  
QY 717 GGTGATTTTGGATCTGCCGCGAAATGAATTTCAACAAAGATGTGTAATGCCAAATCTCCC 776  
Db 421 GGTGATTTTGGATCAGCGCGCTAAGATGAATTCATTAATAA---GGTGGATGCCAAATCTCCC 477  
QY 777 GATT 780  
Db 478 CATT 481

RESULT 7  
LOCUS CN678533 479 bp mRNA linear EST 17-MAY-2004  
DEFINITION E0112C12-5 NTA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12 IMAGE:30777539 5', mRNA sequence.  
ACCESSION CN678533  
VERSION CN678533.1 GI:47444984  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 479)  
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Wang,Y., Carlier,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlesinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.  
TITLE Transcriptional analysis of mouse stem cells and early embryos  
JOURNAL PLOS Biol. 1 (3), 410-419 (2003)  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: E0112 row: C column: 12  
Seq primer: M13 Reverse  
High quality sequence stop: 479  
POLYA=No.

FEATURES  
Location/Qualifiers  
1. 479  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/EvTacr"  
/db\_xref="niaEST:E0112C12-5"  
/db\_xref="taxon:10090"  
/clone="NIA:E0112C12 IMAGE:30777539"  
/sex="Male"  
/tissue\_type="Embryonic Stem Cell"  
/cell\_line="129.3 ES cells"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long)"  
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x103/cm2, on gelatin-coated

plates and cultured for 48 hrs at 37 °C, 5% CO<sub>2</sub>. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an oligo(dT) primer (Invitrogen): 5'-pGATGTTCTAGATCGGAGCGCGCCCTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 25.0%; Score 378; DB 7; Length 479;  
Best Local Similarity 88.0%; Pred. No. 1.2e-103;  
Matches 424; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 297 CGAAGTCAGAAGCTTTGTAGTTGTGGTCACTTTCTGAAGTCAGGTCGTAAGAGAGAA 356  
DB 1 CGAAGTTCGAAGCCTTGTGGCTGTGGTCACTTCCTGAAGTCAGGTCGTAAGAGAA 60  
QY 357 AGCAACCGGGGACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTGGCCAGGA 416  
DB 61 GCGACCGGGGACGCTATGCCATGAATCAATGAAGAAGAGGCTTTGCTGGCCAGGA 120  
QY 417 GCAGGTTTCATTTTGTAGAGAGCGGAACATATTCTCGAAGCACAAGCCGCTGGAT 476  
DB 121 ACAGGTTTCATTTTCGAGGAGAGAGGACATATTCTCGAGCAGAGTCTTGGAT 180  
QY 477 CCCCCATTACAGTATGCTTTTCAGGACAAAATCACTTTATCTGTGTCATGGAATCA 536  
DB 181 CCCCCAGTTACAGTATGCTTTTCAGGACAAAATCACTTTATCTGTGTCATGGAATCA 240  
QY 537 GCTCGAGGGGACTTGTCTCACTTTGAATAGATATGAGGACAGATGATGAACCT 596  
DB 241 GCTCGAGGGGATTTGCTGTCTCTCTGAACATGACGAGGACCAATTAGATGAGCAT 300  
QY 597 GATACAGTTTACCTAGCTAGCTGATTTGGCTGTTTCCAGCGTTCTATCTGATGGATA 656  
DB 301 GATCCAGTTTACCTTGTGAGCTGATTTGGCTGTCCACAGCGTGCCACAGATGGGATA 360  
QY 657 CGTGCATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCT 716  
DB 361 TGTGCATCGAGACATCAAGCCCGAGAACATCTCATGACCGGACGGGACATCAAGCT 420  
QY 717 GGTGATTTTGGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCC 776  
DB 421 GGTGATTTTGGATCAGCGGCTAAGATGAATTCAAATAA---GGTGGATGCCAACTCCC 477  
QY 777 GA 778  
DB 478 CA 479

## RESULT 8

BF562826  
LOCUS 490 bp mRNA linear EST 12-DEC-2000  
DEFINITION UI-R-BJ0p-aip-b-06-0-UI.r1 UI-R-BJ0p Rattus norvegicus cDNA clone  
ACCESSION BF562826  
VERSION BF562826.1 GI:11672556  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 490)

## AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Genome Res. 6 (9), 791-806 (1996)  
97044477  
889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: Bento-soares@uiowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1797673

Seq primer: M13 Forward

Location/Qualifiers

1..490

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BJ0p-aip-b-06-0-UI"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-BJ0p"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ0p

library is a subtracted library derived from the UI-R-AAL,

UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AE1, UI-R-AF1, and

UI-R-AG1 libraries. These libraries represent tissues from

rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal

at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV

canal at 15 dpc, and ventricle at 13 dpc. The tag is a

string of 5-6 nucleotides present between the Not I site

and the oligo-dT track. The library was constructed as

described by Bonaldo, Lennon and Soares, Genome Research

6: 791-806, 1996."

## ORIGIN

Query Match 23.2%; Score 351.4; DB 2; Length 490;  
Best Local Similarity 85.6%; Pred. No. 1.7e-95;  
Matches 391; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 GGGAGATGTTGAAGTTCAAATATGAGCGCGGATTCCTTTGGATGCTGGTCTCTGAA 60  
DB 34 GAGAGATGTTGAAGTTCAAAGTTCAGAGTTCGAGTTCGCGAAACCCGTCGAGCGCCCGGAG 93  
QY 61 CCATTGCCAACCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120  
DB 94 CCATTGCCAGTTCGGGCTCCAGGCTAAATCTCTTCTCCAGGGGAAACCCGCTCTATG 153  
QY 121 ACTCAACAGCAGATGTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTCTTC 180  
DB 154 ACTCAACAGCAGATGTCCTCTTTCCCGGGAAGGGGTGTTAGATGCCCTCTTTCTTC 213  
QY 181 TTTGAGATGAGTCAGCTGCTCTGATGAGATTAGCAGCTGAGCAACTTGTCTCGG 240  
DB 214 TTGGAAGTGCAGTCAGCTGCCCTCATGAAGATAAAGCAGCTGAGCAGCTTGTCTCGG 273  
QY 241 AAGTATTCGACACCATAGCTAGTTACAGGAGCTCCAGCCTTCGCGAAAGACTTCGAA 300  
DB 274 AAGTATTCGACACCATAGCTAGTTACAGGAGCTCCAGCGCTCGGTGAGGACTTCGAA 333  
QY 301 GTCAGAGCTTTGTAGTGTGGTCTACTTCTCTGAGTGCAGGTGTTAAGAGAGAAACA 360  
DB 334 GTGCAAGTCTTGTGGGCTGCGGTCACTTCGCGGAAGTGCAGGTGTTAGAGAGAAGGCC 393

QY 361 ACCGGGACATCTATGCTATGAAGTGTGAGAGAGAGGCTTTATTGGCCGAGGAGCAG 420  
 Db 394 ACCGGGAGTCTACGCCATGAAGATCATGAAGAGGCGCTTTCCGGGCCCCGAGGAGCAG 453  
 QY 421 GTTTCATTTTTCGAGGAGAGCGGAGCATATTTATCTC 457  
 Db 454 GTTTCATTTTTCGAGGAGGAGAGCATATTTATCCC 490

RESULT 9  
 BI654262  
 LOCUS 603280370F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:5310496 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI654262  
 VERSION BI654262.1 GI:15568498  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL1786 row: 1 column: 17  
 High quality sequence stop: 648.

## FEATURES

source  
 Location/Qualifiers  
 1..821  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="NMRI"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5310496"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Mam4"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."

## ORIGIN

Query Match 22.7%; Score 344.2; DB 4; Length 821;  
 Best Local Similarity 84.5%; Pred. No. 3.4e-93;  
 Matches 469; Conservative 0; Mismatches 78; Indels 8; Gaps 7;  
 QY 1 GGGGAGATGTTGAAGTTCAATATGGAGCGCGAATCTTTGGATGCTGCTGCTGAA 60  
 Db 101 GGAGAGATGTTGAAGTTCAAGTATGTGTGCGAACC CGCGAGGCCAGTGCTCCGAG 160  
 QY 61 CCATTGCCAACCGGGCTCCAGGCTGAATCTCTTTTCAGGGGAAACACCTTTATG 120  
 Db 161 CCATTGCCAGTCGGGCTCCAGGCTAAATCTCTTCTCCAGGGGAAACCGGCTCATG 220  
 QY 121 ACTCAACAGCAGATGCTCTCTCTTCCCGAGAGGGATATAGATCCCTCTTTGTC 180  
 Db 221 ACTCAACAGCAGATGCTCTCTCTTCCCGAGAGGGATAGTACGCCCTCTTCGCTCTC 280

QY 181 TTTGAAGAATGCAGTCAGCTCAGCTGCTCTGATGAAGATTAAAGCACGCTGAGCAACTTTGTCCGG 240  
 Db 281 TTGGAAGAGTGCAGCCNAACCCGCCCTGATGAAGATGAAGCACGTCAGCAGCTTAGTCCAG 340  
 QY 241 AAGTATTTCCGACACCATAG-CTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGACTTCGA 299  
 Db 341 AAGTATTTCCGACACCATAGCCCGAGTTGCGGGAGCTGCAGCCCGTCGCGAGAGACTTCGA 400  
 QY 300 A-GTCAGAAGTCTTTGTTAGTTGTTGTTGCTCACTTTGCTGAAGTGCAGGTGG-TAAGAGAGAAA 357  
 Db 401 AGTTTCGAGCCTTGTGGGCTGTGGTCACCTTCGCTGAAGTGCAGGTGGTTCGAGAGAAG 460  
 QY 358 GCAACCCGGGACACTATGCTATGATAAAGTGATGA-AGAAGAAGCTTTATTTGCCCCAGGA 416  
 Db 461 GCGACCCGGGACGCTATATGCTATGCAATGAAATCATGACAGAGAAGGCTTTGTGCCCCAGGA 520  
 QY 417 GCAGGTTTCATTTTTCGAGGAAGAGCGAA-CATATTATCTCGAAGCACAGCCCGCTGGA 475  
 Db 521 ACAGTTTTCATTTTTCGAGGAGAGAGAACCATATATATCTCGAGGACGAGTCTTGA 580  
 QY 476 TCCCCCAATTACAGTATGCTCTTTCAGGA-CAAAAATACCTTTATCTGTCATGG--AAT 532  
 Db 581 TCCACCAAGTTACAGTACGCTTTTCAGGACCAAAAATAAACTTTACCTGGTTCATGGACACT 640  
 QY 533 ATCAGCCTCGAGGGG 547  
 Db 641 ATCAGCCTCGATGGG 655

## RESULT 10

CG501400  
 LOCUS CG501400 450 bp DNA linear GSS 01-OCT-2003  
 DEFINITION OST45250 Mus musculus 129Sv/Ev Mus musculus genomic clone OST45250,  
 genomic survey sequence.  
 ACCESSION CG501400  
 VERSION CG501400.1 GI:37275069  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 450)  
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
 Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
 Fridele,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
 Zhu,Q., Person,C. and Sands,A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: [materials@lexgen.com](mailto:materials@lexgen.com)  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene trap.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST45250"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## FEATURES

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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 /clone="OST45250"  
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 /clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 21.7%; Score 329.2; DB 9; Length 450;  
 Best Local Similarity 90.0%; Pred. No. 1e-88;

Matches 352; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1124 CCCCTTCCTGTTCCACCTCAAGTCGACGATGACACCTCCCAATTTTGATGAACACAGAGA 1183

Db 2 CCCCTTCCTGTTCCACCTCAAGTCGACGATGACACCTCCCAATTTTGATGAACACAGAGA 61

QY 1184 AGAATTCGTGGGTTTCATCTCTCGTGCACCTGAGCCCTCAGCTTCTCGGGTGAAG 1243

Db 62 AGAATTCGTGGGTTTCATCTCTCGTGCACCTGAGCCCTCAGCTTCTCGGGTGAAG 121

QY 1244 AACTGCGCTTTCTGGGGTTTTCGTACAGCAAGCACTGGGATTCCTGTAGATCTGAGT 1303

Db 122 AGTGGCGTTTCTGGGATTTTGTACAGCAAGCACTGGGATTCCTGTAGATCTGAGT 181

QY 1304 CTGTTGTGCGGGTCTGGACTCCCTCGCAAGCTAGCTCCATGAGAAAGAACTTCCTCA 1363

Db 182 CTGTTGTGCGGGTCTGGACTCCCTCGCAAGCTAGCTCCATGAGAAAGAACTTCCTCA 241

QY 1364 TCARAAGCAAGAGCTACAGACTCTCAGGCAAGCTGTCAAGGATTTATTTTCCGAG 1423

Db 242 TCARAAGCAAGAGCTCTCAAGACTCCCAAGCTGTCAAGGATTTATTTTCCGAG 301

QY 1424 CCGGCTCCTCTCTCTGCTCCAGGATCTCCCTCGGTATATGCAAGGATCCGCGGG 1483

Db 302 CCGGCTCCTCTCTCTGCTCCAGGATCTCCCTCGGTATATGCAAGGATCTCCGCGGG 361

QY 1484 GCGGTCTGCTCTGAGCGGCTGATCGT 1514

Db 362 GCGACTGTGTGAGCGGCTGATCGT 392

RESULT 11

BF344814

LOCUS

DEFINITION 602014091F1 NCI\_CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4149886

ACCESSION BF344814

VERSION BF344814.1 GI:11292270

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1993)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LAM9412 row: e column: 23  
High quality sequence stop: 423.

FEATURES

source

1. 423

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="cDNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4149886"

/lab\_host="DH10B (T1 phage-resistant)"

/tissue\_type="gliblastoma with EGFR amplification"

/clone\_lib="NCI CGAP Brn64"

/note="Organ: brain; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: This is a NCI CGAP Library."

Query Match 21.7%; Score 328.8; DB 2; Length 423;

Best Local Similarity 95.7%; Pred. No. 1.3e-88;

Matches 360; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 1 GGGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCTTTGGATGCTGCTGCTGAA 60

Db 48 GGGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCTTTGGATGCTGCTGCTGAA 107

QY 61 CCATTTGCCAACCGCGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTTATG 120

Db 108 CCATTTGCCAGCGCGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTTATG 167

QY 121 ACTCAACAGCAGATGCTCTCTTTCCGAGAGGAGATATAGATGCCCTCTTTGTTCTC 180

Db 168 ACTCAACAGCAGATGCTCTCTTTCCGAGAGGAGATATAGATGCCCTCTTTGTTCTC 227

QY 181 TTTGAAGAATGCACTGAGCTGCTCTG--ATGAAGATTAAAGCACGTC--AGCAACTTTCT 236

Db 228 TTTGAAGAATGCACTGAGCTGCTCTGCAATGCAAGATTAAAGCACGTCGACCACTTTCT 287

QY 237 CCGGAAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGACTT 296

Db 288 CCGGAAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGACTT 347

QY 297 CGAAGTCAGAAGTCTTGTAGTTGGTCACTTCTGTAAGTGCAGGTGTTAAGAGAGA 356

Db 348 CGAAGTCAGAAGTCTTGTAGTTGGTCACTTCTGTAAGTGCAGGTGTTAAGAGAGA 407

QY 357 AGCAACCGGGGACATC 372

Db 408 AGCAACCGGGGACATC 423

RESULT 12

CG501399

LOCUS

DEFINITION CG501399 Mus musculus 129Sv/Ev Mus musculus genomic clone OST45249, genomic survey sequence.

ACCESSION CG501399

VERSION CG501399.1 GI:37275067

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 449)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., Beltrande, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlihauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: [materials@lexgen.com](mailto:materials@lexgen.com)

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. 449

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DEFINITION OST417039, genomic survey sequence.
ACCESSION CG652891
VERSION CG652891.1 GI:37476740
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 512)
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beirand, R., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaling, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
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screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
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Email: materials@lexicon.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
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/db_xref="taxon:10090"
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/clone_lib="Mus musculus 129Sv/Ev"

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Matches 346; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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Db 8 CTCTCTCCCCCTTCG-TCCCCNCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 66

QY 1178 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGAGCTGAGCCCTCAGGCTTCTCGG 1237
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Db 67 CAGAGAAGAAATTCGTGGGTTTCATCTCTCTGTGTCAGCTGAGCCCTCGGCTTCTCAG 126

QY 1238 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGCACTGCGGGAATCTTGGTAGAT 1297
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Db 127 GCGAAGAGCTGCGGTTTGTGGGTTTTCGTACAGCAAGCACTGCGGGAATCTTGGTAGAT 186

QY 1298 CTGAGTCTGTGTGTCGGGTTCTGACTCCCTCCCAAGCTAGCTCCATGGAAGAAAC 1357
      |||||
Db 187 CTGAGTCTGTGTGTCGGGTTCTGACTCCCTCCCAAGCTAGCTCCATGGAAGAAAC 246

QY 1358 TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACCAAGTGTCACAGGTAATTTATTT 1417
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Db 247 TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACCAAGTGTCACAGGTAATTTATTT 306

QY 1418 CCGCAGCGGCTCTCTCTGTCAGGATCTCTCCGTCGATGTCGATGTCGCAAGGATCCG 1477
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Db 307 CCACAGCGGCTCTCTCTGTCAGGATCTCTCCGTCGATGTCGATGTCGCAAGGATCCG 366

QY 1478 CCGGCGGCTCTCTCTGTCAGGATCTCTCCGTCGATGTCGATGTCGCAAGGATCCG 1493
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Db 367 CCGGCGGCTCTCTCTGTCAGGATCTCTCCGTCGATGTCGATGTCGCAAGGATCCG 382

RESULT 14
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DEFINITION BF380737
ACCESSION BF380737
VERSION BF380737.1 GI:11369862
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 340)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
COMMENT 20202663
PUBMED 10737800
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UT0073-
170900-167-H01&t3=2000-09-17&t4=1)
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